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From:

Whiteman, Brian

Sent:

Wednesday, January 11, 2006 6:27 PM

To:

STIC-Biotech/ChemLib

Subject:

seq search

10/822873

SEQ ID NO: 10 and 11

1) us patents and published us patent applications

2) commercial databases

Thanks

Brian Whiteman
Remsen, 2D14
mail box 2C18
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search

NA#_____ AA#:____

S/L:___ Oligomer:____

Encode/Transl:____

Structure #:____Text:___

Inventor:____ Litigation:___

Vendors and cost where applicable STN:

DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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Sequence Sequence

Sequence 2, Appli Sequence 4, Appli Sequence 9, Appli Sequence 4, Appli Sequence 4, Appli Sequence 10631, A Sequence 1440, A Sequence 1, Appli Sequence 3820, Appli

OM protein

Run on:

Sequence:

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JOS-09-033-333-22

Sequence 22, Application US/0903333

Sequence 22, Application US/0903333

Patent No. 6197239

APPLICANT: Wide Chao

APPLICANT: Schurr, Eric
APPLICANT: Honderson, Daniel
TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD

CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 101;
                                US-09-549-519-36
US-08-920-234-2
US-08-920-234-2
US-09-285-502-4
US-09-030-335-9
US-09-031-335-9
US-09-949-016-10631
US-09-949-016-10631
US-09-248-796A-14840
US-09-248-796A-14840
US-08-374-884-1
US-08-374-884-1
US-08-644-271-1
US-08-644-271-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: USA
ZIP: 94304-1018
COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033,333
FILING DATE: 02-MAR-1998
CLASSIFICATION:
PRIOR APPLICATION NUMBER: TELLORICH NUMBER: TILING DATE:
APPLICATION NUMBER: 480.130
REFERENCE/DOCKET NUMBER: 34802-20007.00
TELECHMUNICATION INPORMATION:
TELEPHONE: 650-813-5600
TELEPRAK: 650-813-5600
 .09-489-039A-13241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                             US-10-016-283-1
US-09-134-000C-3820
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
US-09-033-333-22
Query Match
 Sequence 22, Appl
Sequence 23, Appl
Sequence 10; Appl
Sequence 22, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 18, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 8, Appl
Sequence 9, Appl
Sequence 9549, Appl
Sequence 44, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 8267, Ap
Sequence 8, Appli
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                                                                                                                                                                                                                                        1 MTGSTIAPTTDYRNTTATGL......NEKIHRLDGLKPCSLLLQYD 101
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/f_COMB.pep:*

(cgn2_6/ptodata/1/iaa/f_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-09-033-428-23

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US-09-0514-495-20

US-09-151-376-11

US-09-151-376-11

US-09-151-376-11

US-09-11-376-11

US-09-11-376-11

US-09-11-376-11

US-09-11-376-11

US-09-11-351-18

US-09-11-371-18

US-09-11-371-18

US-09-13-371-2

US-09-13-371-371-2

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US-09-10-971-371-2
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                                                                                                                                                                                                                                                                                                                                   572060 segs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
                                                                                                                            January 18, 2006, 19:44:52
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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551
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Perfect score:
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Minimum DB e Maximum DB e

Database

Result Š Searched:

USE

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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                        Sequence 23, Application US/09033428
Sequence 23, Application US/09033428
Setent No. 625462
GENERAL INFORMATION:
APPLICANT: Little, Andrew
APPLICANT: Little, Henry
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLLIMWLIC 60
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                                                                                              1 MIGSTIAPTIDYRNITATGLISALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
                                                                    1 MIGSTIAPITDYRNITATGLISALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
                         Gaps
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                         0; Indels
                                                                                                                                                           61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                         61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EL POPPY disk
COMPUTER: EL PER PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033,428
FILLNG DATE:
CLASSIFICATION:
Best Local Similarity 100.0%; Pred. No. 6.9e-60; Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: POLIZZI, CATHERINE M.
REGISTRATION NUMBER: 40,130
REEFERENCE/DOCKET NUMBER: 34802-30004.00
TELEPHONE: (415) 815-5600
TELEPHONE: (415) 815-5600
TELERAX: (415) 814-0792
TELEX: 706141 MRSNFORES SFO
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 101 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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US-09-033-556-10 ; Sequence 10, Application US/09033556 ; Patent No. 6432700

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Schuur, Eric
Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
THEREOF
APPLICANT: Henderson, Daniel R.
APPLICANT: How Chao
TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
TITLE OF INVENTION & FORESTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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100.0%; Score 551; DB 2;
Best Local Similarity 100.0%; Pred. No. 6.9e-60;
Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                             COMPUTER: In Comparible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34802-20010.00
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ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/09614495
Patent No. 6436394
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Catherine, Polizzi M
REGISTRATION UNUBER: 40,130
REFERENCE/DOCKET NUMBER: 3480
TELECOMMUNICATION INFORMATION:
TELEFRAX: 650-494-0792
TELEY. 706141
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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1 MTGSTIAPTTDYRNTTATGLISALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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FILING DATE: 02-Jul-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION: «Unknown»
PRIOR APPLICATION: ADATE: ALMENOWN»
APPLICATION NUMBER: US/09/033,428
FILING DATE: «Unknown»
ATONES/AGENT INFORMATION:
NAME: POLIZZI, CATHERINE M.
REGISTRATION NUMBER: 34802-30004.00
REFERENCE/DOCKET NUMBER: 34802-30004.00
TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 913-5600
TELEPRAX: (415) 940-0792
TELERX: 706141 MRSNPOERS SFO
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
TYRE: AMINO acids
TYRE: AMINO acids
TYRE: AMINO acids
TYRE: AMINO acids
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Patent No. 6676935
GENERAL INPORMATION:
APPLICANT: Henderson, D.R.
TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
FILE REFERENCE: 34802200221
CURRENT PILING DATE: 1998-09-10
FEARLIER APPLICATION NUMBER: US/69/151,376
CURRENT FILING DATE: 1996-06-26
EARLIER PILING DATE: 1996-06-26
EARLIER PILING DATE: 1995-06-27
SEQIER FILING DATE: 1995-06-27
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
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ORGANISM: Homo sapiens
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US-09-814-351-18
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US-09-151-376-11
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Sequence 23, Application US/0989883
Patent No. 6585968
GENERAL INFORMATION:
APPLICANT: Little, Andrew
Lamparski, Henry
Schuur, Eric
Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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ZIP: 9304-1018
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                      COMPUTER READABLE FORM:

MEDIUW TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/614,495
FILING DATE: 11-Jul-2000
CLASSIFTCATION: cubrnown>
PRIOR APPLICATION: cubrnown>
PRIOR APPLICATION: cubrnown>
PRIOR APPLICATION: cubrnown>
APPLICATION NUMBER: 09/033,333
FILING DATE: Cubrnown>
APPLICATION NUMBER: 09/033,333
FILING DATE: Cubrnown>
TELERROWINICATION: INFORMATION:
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; FLENGTH: 101 amino acids
; TYPE: amino acids
; TYPE: amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGNENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-614-495-22
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APPLICATION NUMBER: US/09/898,883
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ADDRESSEE: MORRISON & FOERSTER
STREET 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 23
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US-09-898-883-23
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61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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US-09-875-228-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT: Yu, De-Chao
APPLICANT: Zhang, Hong
APPLICANT: Zhang, Hong
APPLICANT: ALAng, Hong
APPLICANT: Henderson, Daniel R.
TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 348022001500
CURRENT APPLICATION NUMBER: 06/191,861
PRIOR PLILNG DATE: 2001-10-12
RIOR APPLICATION NUMBER: 60/191,861
PRIOR PLILNG DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 46
SSOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MIGSTIAPTIDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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                   GENERAL INFORMATION:
APPLICANT: Yu, De-Chao
APPLICANT: Yu, De-Chao
APPLICANT: Henderson, Daniel R.
TITLE OF INVENTION: CEAL-SPECIFIC ADENOVIRUS VECTORS
CURRENT APPLICATION NUMBER: US/09/814,351
CURRENT APPLICATION NUMBER: 60/192,156
PRIOR PRING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PRESENCE 535
SOFTWARE: PRESENCE FRIENCE MINDOWS VERSION 4.0
SEQ ID NO 18
LENGTH: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 551; DB 2; Length 101; 100.0%; Pred. No. 6.9e-60; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CLKRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Amino acid sequence for ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Amino acid sequence for ADP
US-09-814-292-4
  Sequence 18, Application US/09814351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09814292
Patent No. 6852528
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 101; Conservative
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LENGTH: 101
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GENERAL INCLORNATION.

JAPPLICANT: Henderson, D.R.

APPLICANT: Henderson, D.R.

APPLICANT: Henderson, D.R.

APPLICANT: SCHUARY

TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE

TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF

TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF

TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF

TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF

TITLE OF INVENTION NUMBER: US/09/875,228

CURRENT APPLICATION NUMBER: 00/012,834

PRIOR FILING DATE: 1998-08-03

PRIOR FILING DATE: 1998-04-03

PRIOR PILING DATE: 1998-04-04

NUMBERS OF SEQ ID NOS: 38

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 101

TYPE: PRI

TYPE: PR
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Sequence 18 Application US/09814357

Patent No. 6911200

GENERAL INFORMATION:
APPLICANT: TV, De-Chao
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REPERENCE: 34802201600
CURRENT APPLICATION NUMBER: US/09/814,357
CURRENT APPLICATION NUMBER: 60/192,015
PRIOR APPLICATION NUMBER: 60/192,015
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 18
LENGTH: 101

LENGTH: 101
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Best Local Similarity 100.0%; Pred. No. 6.9e-60;
Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 551; DB 2; 100.0%; Pred. No. 6.9e-60;
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Patent No. 6916918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
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Matches 101; Conservative
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Sequence 29549, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 9549
ILENGTH: 521
                                                                                                       4 STIAPTIDYRNTTATGLTS-ALNLPQVHAFVND-----WASL-DMWWFSI---ALMFVC 52
                                                                   24 INLPQVHAFVNDWASLDMW---WFSIALM-----FVCLIIMWLICCLKRRRARPPIYRP
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Patent No. 6852837

GENERAL INPORMATION:

APPLICANT: Busicial Samantha J.

TITLE OF INVENTION: NOVEL MOLECULES OF THE

TITLE OF INVENTION: HERPENSYLRUS-ENTRY-MEDIATOR-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: MBIO98-061CP1CN1 (M)

CURRENT PELING DATE: 2001-08-21

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-06-39

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FRELEE 1998-09-03

NUMBER OF SEQ ID NOS: 58

SEQ ID NO 44

LENGTH: 239
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Best Local Similarity 35.9%; Pred. No. 1.3;
Matches 14; Conservative 10; Mismatches 11; Indels
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19;
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Mismatches
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21; Conservative
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US-09-934-289A-44
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APPLICANT: Yu, De Chao
TITLE OF INVENTION: Status-Specific Response Elements and Methods of Use Thereof
FILE REFERENCE: CELL-014; 122, 822A
CURRENT FILING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: 06/099,791
PRIOR PLING DATE: 1998-09-10
PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 95
LENGT
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| GENERAL INFORMATION:
| APPLICANT: TORDO, NOEL
| APPLICANT: PERRIN, PIERRE
| APPLICANT: PERRIN, PIERRE
| APPLICANT: BAHLOUL, CHOKRI
| TITLE OF INVENTION: CHIMERIC LYSSAVIRUS NUCLEIC ACIDS AND POLYPEPTIDES
| TITLE OF INVENTION CHIMERIC LYSSAVIRUS NUCLEIC ACIDS AND POLYPEPTIDES
| CURRENT APPLICATION NUMBER: 08/09/549,519
| CURRENT PLIANG DATE: 1999-04-14
| PRIOR PILING DATE: 1999-04-15
| NUMBER OF SEQ ID NOS: 40
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 33
| LENGTH: 522
                                1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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Pred. No. 1.5;
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                                                                                                                                                                       61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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Best Local Similarity
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US-09-549-519-33
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12.9%; Score 71; DB 2; Length 277;
Best Local Similarity 35.9%; Pred. No. 1.6;
Matches 14; Conservative 10; Mismatches 11; Indels
RESULT 15
US-09-934-289A-42
Sequence 42. Application US/09934289A
Fatent No. 6852837
Fatent No. 6852837
Fatent No. 6852837
FILE OF INVENTION: HEREBYLEUES OF THE
TITLE OF INVENTION: HEREBYLEUES OF THE
TITLE OF INVENTION: HEREBYLEUES OF THE
FILE REFERENCE: MIJO98-061CPLCN1(M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR PILING DATE: 2999-06-29
PRIOR PILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 42
LENGTH: 277
LENGTH: 277
LENGTH: 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: SIGNAL
LOCATION: (1) ... (38)
US-09-934-289A-42
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Search completed: January 18, 2006, 19:48:54 Job time : 23 secs

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JS-09-392-822-9
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680.657 Million cell updates/sec
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1 MTGSTIAPTTDYRNTTATGL......NEKIHRLDGLKPCSLLLQYD 101
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-09-814-292-4

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US-09-814-351-18

US-10-045-116-20

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US-10-938-22-8

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 4, Application US/09814292

Sequence 4, Application US/09814292

Patent No. US20020120117A1

GENERAL INFORMATION:

APPLICANT: YU, De-Choo

APPLICANT: Alang, Hong

APPLICANT: Alang, Hong

APPLICANT: Henderson, Daniel R.

TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN

TITLE OF INVENTION: WETANSCRIPTIONAL REGULATORY SEQUENCES, AND

TITLE OF INVENTION: METHODS OF USE THEREOF

TITLE OF INVENTION: METHODS OF USE THEREOF

TITLE REPERRENCE: 340022001500

CURRENT APPLICATION NUMBER: US/09/814,292

CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yu, De Chao
APPLICANT: Yu, De Chao
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: Adenovirus Vectors Containing Cell
TITLE OF INVENTION: Status-Specific Response Elements and Methods of Use Thereof
FILE REFERENCE: 348022001200
CURRENT APPLICATION NUMBER: US/09/392,822
CURRENT FILING DATE: 1999-09-09
EARLIER APPLICATION NUMBER: 60/099,791
EARLIER FILING DATE: 1998-09-10
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 9
SEQ ID NO 9
SEQ ID NO 9
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Sequence 6, Appli
Sequence 203585,
Sequence 203646,
Sequence 900, App
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550, App
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470, Appl
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59454, A
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                                  US-10-322-281-550
US-10-614-853-12
US-10-614-853-12
US-10-932-991-13
US-10-939-359-2
US-10-943-199-48
US-10-775-204-470
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US-10-282-122A-59454
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US-10-282-122A-59454
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US-10-437-963-203585
US-10-437-963-203646
US-10-732-923-900
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100.0%; Score 551; DB 3;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0;
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ORGANISM: Adenovirus V
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| Sequence 5. Application US/09875228
| Patent No. US20020136707A1
| GENERAL INFORMATION:
| APPLICANT: Yu, D. |
| APPLICANT: Henderson, D.R. |
| APPLICANT: Schuur, E.R. |
| TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF |
| TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF |
| TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF |
| TILLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF |
| FILE REPERENCE: 348022000900 |
| CURRENT APPLICATION NUMBER: US/09/875,228 |
| CURRENT PLILING DATE: 1998-08-03 |
| PRIOR FILING DATE: 1998-08-03 |
| PRIOR FILING DATE: 1998-03-02 |
| PRIOR FILING DATE: 1998-03-05 |
| SOFTWARE: PATENTIN VET: 2.0 |
| SOFTWARE: PATENTIN VET: 3.0 |
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Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels (
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PRIOR APPLICATION NUMBER: 60/191,861
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 101
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Patent No. US20020164799A1
GENERAL INFORMATION:
APPLICANT: Little, Andrew
Lamparski, Henry
Schuur, Eric
                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 101; Conservative
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ORGANISM: Adenovirus
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Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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                                                                                                                                                                                                                             COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,883
FILING DATE: 02-Jul-2001
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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APPLICANT: Schuur, B.R.
TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
FILE REPERRACE: 348022000221
CURRENT APPLICATION NUMBER: US/09/151,376
CURRENT FILING DATE: 1998-09-10
BARLIER FILING DATE: 1996-06-26
BARLIER FILING DATE: 1996-06-27
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PALENTH: Ver: 2.0
SOFTWARE: PALENTH: Ver: 2.0
SOFTWARE: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: POLIZZI, CATHERINE M.
REGISTRATION NUMBER: 40, 130
REFERENCE/DOCKET NUMBER: 34802-30004.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-898-883-23
                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSER: MCRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 706141 MRSNFOERS SFO INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-151-376-11
; Sequence 11, Application US/09151376
; Publication No. US/0030044383A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 101 amino acids
                                                                                 NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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US-10-045-116-20
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                                                                                                                                                                                 1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yu, De-Chao
APPLICANT: Yu, De-Chao
APPLICANT: Chen, Yu
APPLICANT: Chen, Yu
APPLICANT: Henderson, Daniel R.
TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA
TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,
TITLE OF INVENTION: CHEWOTHERAPY AND RADIATION
FILE REFERENCE: 348022001600
CURRENT APPLICATION NUMBER: US/09/814,357
CURRENT PILLING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 60/192,015
PRIOR APPLICATION NUMBER: 60/192,015
PRIOR FILLING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PARESEQ FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yu, De-Chao
APPLICANT: Yu, Yuanhao
APPLICANT: Li, Yuanhao
APPLICANT: Handerson, Daniel R.
ATTLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME BNTRY SITE
TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME BNTRY SITE
TITLE OF INVENTION NUMBER: 05/09/814,351
CURRENT APPLICATION NUMBER: 60/192,156
PRIOR APPLICATION NUMBER: 60/192,156
PRIOR APPLICATION NUMBER: 60/192,156
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FRAELSEQ for Windows Version 4.0
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                                                                            Length 101;
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                                                                                                                                                                                                                                                                                CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                           61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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                                                                          100.0%; Score 551; DB 3;
100.0%; Pred. No. 8.2e-56;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 551; DB 3;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Amino acid sequence for ADP US-09-814-357-18
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-814-357-18
; Sequence 18, Application US/09814357
; Publication No. US20030068307A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application US/09814351
Publication No. US20030148520A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                    Query Match
Best Local Similarity 100.
Matches 101, Conservative
; ORGANISM: Homo sapiens
US-09-151-376-11
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LENGTH: 101
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APPLICANT: Lamparski, Henry
Schuur, Eric
Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
THEREOF THEREOF
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                                                                                                                                                                                                                                                 1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
                                                                                                                                                                                                         Gaps
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                                                                                                                                                             Length 101;
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COMPUTER READABLE FORM:
MUEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPALIDLE
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/10/045,116
FILING DATE: 23-Oct-2001
CLASSIFICATION: (Unknown)
PRIOR APPLICATION OBTA:
APPLICATION NUMBER: US/09/033,555A
ATTORNEY/AGENT INFORMATION:
NAME: POLIZZI, CATHERINE M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-30005.00
TELEPHONE: (415) 013-5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                CLKRRRARPELYRPIIVLNPHNEKIHRLDGLKPCSLLLLQYD 101
                                                                                                                                                        100.0%; Score 551; DB 3;
Similarity 100.0%; Pred. No. 8.2e-56;
01; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 551; DB 4;
100.0%; Pred. No. 8.2e-56;
ive 0; Mismatches 0;
; LENGTH: '101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence for ADP
US-09-814-351-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-045-116-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 706141 MRSNFOERS SFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES:
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/10045116 Publication No. US20030026792A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 101 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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Best Local Similarity 100.09
Matches 101; Conservative
                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 101; Conservative
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Henderson, Daniel
TITLE OF INVENTION: ADBNOVIRUS VECTORS SPECIFIC
FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS
OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                       CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CLKRRRARPPIYRPIIVLNPHNBKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/222,479
FILING DATE: 16-Aug-2002
CLASSIFICATION SUMBER: US/09/614,495
RIORICATION NUMBER: US/09/614,495
FILING DATE: 11-Jul-2000
APPLICATION NUMBER: US/09/33,333
FILING DATE: US-2000
APPLICATION NUMBER: US/09/31,333
FILING DATE: UNFORMATION:
ATORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 4602-20007.00
TELECOMMUNICATION INFORMATION:
                                                                 61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRACMENT TYPE: Înternal
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-222-479-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                             Sequence 22, Application US/10222479
Publication No. US20030091538A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 101 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650-494-0792
TELEX: 706141
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                                                                                                                                                                                                                                                                         APPLICANT: Yu, De Chao
Schuur, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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Best Local Similarity 100.
Matches 101; Conservative
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                                                                                                                                                                      RESULT 9
US-10-222-479-22
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Sequence 271104, Application US/10425115
Sequence 271104, Application US/10425115
Sequence 271104, Application US/10425115
Sequence 271104, Application US/040214272A1
Sequence 271104, Application No. 220040214272A1
SEMENAL INFORMATION: Thomas J.
APPLICANT: Zoo, Yougwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
SETILE REFERENCE: 38-21 (52222) B
CURRENT APPLICATION NUMBER: US/10/425,115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 LNLPQVHAFVNDWASLDMW---WFSIALM-----FVCLIIMWLICCLKRRRARPPIYRP 74
                                                                                                                                                                                                                                                                                                                                           7 APTIDYRNTIATGLISALNIPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLICCLKRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Indels 12; Gaps
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                                                                                                                                                                                                                                                  Length 95;
                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                  94.7%; Score 522; DB 5; 1
100.0%; Pred. No. 1.7e-52;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   67 ARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 95
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/392,822
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 33, Application US/10608538 Publication No. US20050064389A1
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Laginga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Lyssavirus sp.
                                                                                                                                                         TYPE: PRT
ORGANISM: Adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-608-538-33
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Publication No. US20050169890A1
GENERAL INFORMATION:
APPLICANT: Yu, Deniel
TITLE OF INVENTION: Adenovirus Vectors Containing Cell
TITLE OF INVENTION: Status-Specific Response Elements and Methods of Use Thereof
FILE REFERENCE: CELL-014; 122.1
CURRENT APPLICATION NUMBER: US/10/938,227
CURRENT FILING DATE: 2004-09-09
                                                                                                                                                                                                                                                                         MIGSTIAPTIDYRNTIATGLISALNIPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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                                                                                                                                                         Length 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence II. Application US/10822873

Publication No. US20040241857A1

GENERAL INFORMATION:
APPLICANT: Henderson, D.R.
APPLICANT: Henderson, D.R.
TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS
FILE REFERENCE: CELL-004C002,
CURRENT APPLICATION NUMBER: US/10/822,873
FRICH APPLICATION NUMBER: 09/732,169
PRIOR FILING DATE: 2000-12-06
PRIOR PILING DATE: 2000-12-06
PRIOR PILING DATE: 1998-09-10
PRIOR PILING DATE: 1998-09-10
PRIOR FILING DATE: 1996-06-26
PRIOR FILING DATE: 1996-06-26
PRIOR FILING DATE: 1995-06-27
NUMBER OF SEQ IN DOS: 71
SOFTWARE PARENTIN VET. 2.0
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                                                                                                                                                       100.0%; .Score 551; DB 4;
100.0%; Pred. No. 8.2e-56;
iive 0; Mismatches 0;
                                                                                      ; OTHER INFORMATION: Amino acid sequence for ADP US-10-691-045-18
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                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                   Matches 101; Conservative
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                                                                                                                                                       Query Match
Best Local Similarity
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Best Local Similarity
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US-10-822-873-11
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  LENGTH: 101
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APPLICANT: Scalato, Enzo
APPLICANT: Masignani, Vega
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-212-443-174
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Sequence 1199, Ap
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Sequence 64, Appli
Sequence 64, Appli
Sequence 141, Appli
Sequence 510, Appli
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Sequence 6656, Appli
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Sequence 175, App
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113.725 Million cell updates/sec
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                                                                                                                                                         1 MTGSTIAPTTDYRNTTATGL......NEKIHRLDGLKPCSLLLQYD 101
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(cgnZ 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

(cgnZ - f)ptodata/1/pubpaa/USO6 NEW PUB.pep:*

(cgnZ 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

(cgnZ 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

(cgnZ 6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-11-212-443-174

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US-10-6213-7443-1199

US-10-353-783-50

US-10-353-783-50

US-10-966-648-2

US-10-966-648-2

US-10-966-648-2

US-11-139-443-360

US-11-139-443-360

US-11-212-443-141

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US-11-052-554A-141

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Maximum Match 100%
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Maximum DB seq length: 200000000
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Match 1
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Perfect score:
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Fublication No. US20050272118A1
GENERAL INFORMATION:
APPLICANT: CLARK, HILARY
APPLICANT: CLARK, HILARY
APPLICANT: CLARK, HILARY
APPLICANT: GENENIC BRIDD
APPLICANT: WRANIK, BERND
APPLICANT: GONZALES, LINO
APPLICANT: OUYANG, WENUN
APPLICANT: OUYERTION: Immune Related Diseases
TITLE OF INVENTION: Immune Related Diseases
TITLE OF INVENTION: NUMBER: US/10/987,663
CURRENT APPLICATION NUMBER: US 60/421,236
FRIOR FILING DATE: 2004-11-12
FRIOR APPLICATION NUMBER: US 60/421,236
FRIOR PILING DATE: 2003-10-25
FRIOR FILING DATE: 2003-02-19
NUMBER OF SEQ ID NOS: 10
SEQ ID NOS: 10
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                 US-11-165-160-2
US-11-055-822-586
US-10-465-822-586
US-11-148-012-2
US-10-661-426-4
US-10-661-426-13
US-10-661-426-13
US-10-081-234-1648
US-11-000-463-259
US-11-101-387-18
US-10-13-837-18
US-11-113-837-18
US-11-191-376-4
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US-10-454-437-278
US-11-174-150-29
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Publication No. US20050287165A1
GENERAL INFORMATION:
APPLICANT: Scalato, Enzo
APPLICANT: Masignani, Vega
APPLICANT: Rappuoli, Rino
TYPE: PRT
ORGANISM: Homo sapiens
US-10-987-663-4
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LOCATION: (170)
OTHER INFORMATION: absent or positive
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OTHER INFORMATION: absent or positive FEATURE: STE
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NAME/KEY: SITE
LOCATION: (101)
OTHER INFORMATION: absent or positive
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LOCATION: (163)
OTHER INFORMATION: absent or positive
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LOCATION: (166)
OTHER INFORMATION: absent or positive
                                        LOCATION: (53)..(67)
OTHER INFORMATION: absent or positive
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LOCATION: (109)
OTHER INFORMATION: absent or positive
PERTURE:
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NAME/KEY: SITE
(137)
OTHER INFORMATION: absent or positive
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THER INFORMATION: absent or positive
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OTHER INFORMATION: absent or positive
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OTHER INFORMATION: absent or positive
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OTHER INFORMATION: absent or positive
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OTHER INFORMATION: absent or positive
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OTHER INFORMATION: absent or positive
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LOCATION: (155)..(156)
OTHER INFORMATION: absent
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LOCATION: (104)
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NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
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11.3%; Score 62.5; DB 7; Length 222;
Best Local Similarity 25.2%; Pred. No. 1.4;
Matches 26; Conservative 15; Mismatches 37; Indels 2.
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OTHER INFORMATION: Description of Artificial Sequence: ORF39
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| Publication No. US20050287165A1 |
| GENERAL INPORMATION: | APPLICANT: Scalato, Enzo APPLICANT: Masignani, Vega APPLICANT: Masignani, Vega APPLICANT: Pizza, Mariagrazia APPLICANT: Erandi, Guido | TITLE OF INVENTION: Meningococcal Antigens | FILE REFERENCE: CHRRO159 | CURRENT APPLICATION NUMBER: US/01/212,443 | CURRENT APPLICATION NUMBER: US/09/302,626 | PRIOR FILING DATE: 1999-04-30 | PRIOR FILING DATE: 1999-01-14 | NUMBER OF SEQ ID NOS: 195 | SOFTWARE: Patentin Ver. 2.1 | SEQ ID NO 175 | LENGTH: 222
FILE REFERENCE: CHIR0159
CURRENT APPLICATION NUMBER: US/11/212,443
CURRENT FILING DATE: 2005-08-24
FRIOR APPLICATION NUMBER: US/09/302,626
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-01-14
FRIOR PILING DATE: 1999-01-14
FRIOR PILING DATE: 1999-01-14
FRIOR PILING DATE: 1999-01-14
FRIOR APPLICATION NUMBER: PCT/1B99/00103
FRIOR PILING DATE: 1999-01-14
FRIOR FILING DATE: 1999-01-14
FRIOR FILING DATE: 1999-01-14
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OTHER INFORMATION: absent or positive
PEATURE:
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; OTHER INFORMATION: place-holder
US-11-212-443-174
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LOCATION: (17)..(33)
OTHER INFORMATION: place-holder
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NAME/KEY: SITE
LOCATION: (53).. (67)
OTHER INFORMATION: place-holder
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ORGANISM: Artificial Seguence
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NAME/KEY: SITE
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Sequence 1199, Application US/10821234

Sequence 1199, Application Worl02080255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT APPLICATION NUMBER: US 60/462,047

PRIOR PRIOR PILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: PL SEQ Genes Version 1.0

SEQ ID NO 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 APENNEKTKEFWSTYTKAQQGESNRGSDWFQFYLTFPLIFGLFILLUVFLIWRCFLRNK 123
                                                                                                                                                                                                                                       ---WFSIAL------MFVCLIIMWLI--CCLKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
                                                                                                                  10.4%; Score 57.5; DB 6; Length 1196; 19.7%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.3%; Score 57; DB 6; Length 232; 21.6%; Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Indels
                                                                                                                                                                                                        12 YRNTTATGLTSALNLPQVHAFV------NDWASLDMWWFSIA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 TRROTVTEGHIPFPQHLNIITPPPPPDEVFDSSGLSP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 RARP------PIYRPIIVLNPHNEKIHRLDGLKP 93
                                                                                                                                                              17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 50, Application US/10353783
Publication No. US20050261175A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 AFVNDWASLDMW------
                                                                                                                                                                 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 21.69
Matches 21; Conservative
                                                                                                                                                                                                                                                                                               51 VCLIIMWLICC 61
                                                                                                                                                                                                                                                                                                                                           71 RTLKYLWTVCC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1199
                         TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                  Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-821-234-1199
    LENGTH: 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-353-783-50
                                                                        US-10-613-744-9
                                                                                                                    Query Match
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Sequence 9, Application US/10613744

Publication No. US20050272093A1

GENERAL INFORMATION:
APPLICANT: The Rockefeller University
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Cation Channel Proteins, and Uses Thereof
FILE REFERENCE: 018512-002901US
CURRENT APPLICATION NUMBER: US/10/613.744
CURRENT PILING DATE: 1999-03-24

PRIOR FILING DATE: 1999-03-24

PRIOR FILING DATE: 1999-04-02

PRIOR APPLICATION NUMBER: US 09/045,529

PRIOR FILING DATE: 1999-04-02

PRIOR APPLICATION NUMBER: WO PCT/US99/06307

PRIOR FILING DATE: 1999-03-22

NUMBER OF SEQ ID NOS: 42

SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 GDTVARVRELXQIRNFLTGQALTSXLDLXFSF1F----XAVMWYYSXXLTXVVLXSLXC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GSTIAPTTD---YRN-TTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 ICCLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.8%; Score 59.5; Di
Best Local Similarity 25.2%; Pred. No. 3.3;
Matches 26; Conservative 13; Mismatches
LOCATION: (192)
OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                                                            LOCATION: (203)..(204)
OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (209) .. (212)
OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (216)
OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i LOCATION: (219)...(220)
i OTHER INFORMATION: absent or positive US-11-212-443-175
                                                                                                                                                                                                                                                                                               OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
LOCATION: (214)
OTHER INFORMATION: absent or positive
                                                                                                                OTHER INFORMATION: absent or positive
                                                                                                                                                                                 LOCATION: (199)
OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: SITE
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                                                                                           LOCATION:
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                                                                                                                                       FEATURE:
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Sequence 27, Application US/10966648

Publication No. US20050249734A1

GENERAL INFORMATION:
APPLICANT: Succliffe, J. Gregor
APPLICANT: Henriksen, Steven J.
APPLICANT: Henriksen, Steven J.
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods
FILE REFERENCE: 14740A-0006640US
CURRENT APPLICATION NUMBER: US/10/966,648
CURRENT FILING DATE: 2004-10-14
PRIOR FILING DATE: 1996-06-15
PRIOR FILING DATE: 1996-06-15
PRIOR FILING DATE: 1997-06-15
PRIOR FILING DATE: 2001-01-18
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 103
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Sequence 2, Application US/1096648

Publication No. US20050249734A1

GENERAL INFORMATION:
APPLICANT: Sutcliffe, J. Gregor
APPLICANT: de Lecea, Luis
APPLICANT: Henriksen, Steven J.
APPLICANT: Siggins, George R.
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: positions 10-112 of rat preprocortistatin (CST) OTHER INFORMATION: cortistatin-29
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10.2%; Score 56; DB 6; Length 103;
Best Local Similarity 36.4%; Pred. No. 3.8;
Matches 12; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                               DB 6; Length 85;
3;
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                                                                                                                                                                                                                                                                                                                                 ; Score 56; DB 6
; Pred. No. 3;
5; Mismatches
PRIOR FILING DATE: 1997-05-15
PRIOR PEDIGACHON NUMBER: US 09/766,396
PRIOR FILING DATE: 2001-01-18
NUMBER OF SEQ ID NOS: 31
SEG ID NO 6
LENGTH: 85
                                                                                                                                                                                                                                                     ) OTHER INFORMATION: rat procortistatin US-10-966-648-6
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 36.4%;
Matches 12; Conservative
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ORGANISM: Rattus sp.
FEATURE:
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Publication No. US20050249734A1

GENERAL INFORMATION:

APPLICANT: Sutcliffe, J. Gregor

APPLICANT: Ge Lecea, Luis

APPLICANT: Henriksen, Steven J.

APPLICANT: The Scripps Research Institute

TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods

FILE REFERENCE: 14740A-000640US

CURRENT APPLICATION NUMBER: US/10/966,648

CURRENT FILING DATE: 1996-05-15

PRIOR PILING DATE: 1996-05-15

PRIOR APPLICATION NUMBER: US 08/648,322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 VVSSTLSPEKDSR----VSVTKPFMLPPVAASSLRNDSSSSNRKAKNPTGDSSLHWAAMA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.3%; Score 57; DB 6; Length 273; 26.0%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 LPAFFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISML 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHA--FVNDWASLD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 L-MFVCLIIMWLICCLKRRARPPIYRPI--IVLNPHNEKIHRL 88
                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32958A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Mismatches
                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1955
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-ARR-1991
APPLICATION NUMBER: 07/684,535
FILING DATE: 01-ARR-1991
APPLICATION NUMBER: 07/689,701
FILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/593,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-353-783-50
                                                                                                                                                      FILING DATE: 28-Jan-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 273 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 26.0%
Matches 27; Conservative
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Gaps

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2 TGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMW--WF-----SIALMF 50
                                                                               FRIOR APPLICATION NUMBER: US 60/141031
FRIOR APPLICATION NUMBER: US 60/141031
FRIOR PELING DATE: 1999-06-25
FRIOR PELING DATE: 1999-06-25
FRIOR PELING DATE: 1999-06-26
FRIOR FILING DATE: 1999-07-08
FRIOR FILING DATE: 1999-07-08
FRIOR FILING DATE: 1999-07-09
FRIOR FILING DATE: 1999-07-04
FRIOR FILING DATE: 1999-07-04
FRIOR FILING DATE: 1999-07-04
FRIOR FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.2%; Score 56; DB 6; Length 1274; Best Local Similarity 20.2%; Pred. No. 59; Matches 18; Conservative 21; Mismatches 28; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 VHAFVNDWASL-DMWW----FSIALMFVCLIIMWLICCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55; DB 6;
Pred. No. 5.5;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1110 ITVVMKW-VCVGKHKPSEHPLFSRFVWLN 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 VCLIIMWLICCLKRRRARPPIYRPIIVLN 79
                                       CURRENT APPLICATION NUMBER: US/10/454,437
CURRENT FILING DATE: 2003-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Corynebacterium glutamicum
US-10-454-437-360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-467-657-5542
; Sequence 5542, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Neisseria gonorrhoeae US-10-467-657-5542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 27.5%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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Publication No. US20050277115A1

GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Aberhauer, Gregor
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Indels 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.2%; Score 56; DB 6; Length 112; 36.4%; Pred. No. 4.1; tive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fann, Ming-Ji
TITLE OF INVENTION: Cellular Proliferation Control Factors
FILE REFERENCE: 1774-1002001
FILE REFERENCE: 1774-1002001
CURRENT APPLICATION NUMBER: US/11/139,435
CURRENT FILING DATE: 2005-05-27
PRIOR APPLICATION NUMBER: US 60/575,611
PRIOR FILING DATE: 2004-05-27
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 LKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPC 94
FILE REFERENCE: 14740A-000640US
CURRENT APPLICATION NUMBER: US/10/966,648
CURRENT FILING DATE: 2004-10-14
PRIOR APPLICATION NUMBER: US 08/648,322
PRIOR APPLICATION NUMBER: US 08/657,389
PRIOR PILING DATE: 1996-05-15
PRIOR APPLICATION NUMBER: US 09/766,396
PRIOR FILING DATE: 1997-05-15
PRIOR FILING DATE: 2001-01-18
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: rat preprocortistatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/11139435; Publication No. US20050287664A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SIGNAL
LOCATION: (1)..(27)
CHER INFORMATION: signal peptide
02-10-966-648-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 36.44
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 30.4*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: M. musculus
US-11-139-435-2
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-10-454-437-360
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LENGTH: 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-11-139-435-2
                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
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22; Gaps

2 Gaps . 9 APPLICANT: CHIRON SpA
APPLICANT: CHIRON SpA
APPLICANT: POTTANA Maria Rita
APPLICANT: POTTANA Maria Rita
APPLICANT: POTTANA Mariagrazia
APPLICANT: MASIGNAI Vega
APPLICANT: MASIGNAI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REPERSICE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT PILING DATE: 2003-08-11
PRIOR PILING DATE: 2001-02-12
NUMBER: OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 5542
LENGTH: 113 DB 6; Length 113; Indels 15;

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US-11-052-554A-141

Sequence 141, Application US/11052554A

Publication No. US20050288866A1

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION:

TOTALE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TOTALE OF INVENTION:

TITLE OF INVENTION:

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117 TGSTVSSPEGRNTVTAKXIDVEFANNRYATDYAHTQEQKGLTVALNVPVVQAAQN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TTDYRNT-TATGLTSALNLPQVHAFVN 34
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Pred. No. 34;
                                                                                     221 LPAFFSLVIGFAFGALYWKKKQPNLTRTVENIQINEEDNEISML 264
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                                      48 L-MFVCLIIMWLICCLKRRRARPPIYRPI--IVLNPHNEKIHRL
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                                                                                                                                                                                                                                                                               Sequence 64, Application US/11212443
| Schence 64, Application US/11212443
| Publication No. US20050287165A1
| GENERAL INFORMATION:
| APPLICANT: Scalato, Enzo
| APPLICANT: Masignani, Vega
| APPLICANT: Pizza, Mariagrazia
| APPLICANT: Pizza, Mariagrazia
| APPLICANT: Grandi, Guido
| TITLE REFERENCE: CHIROLS9
| CURRENT APPLICATION NUMBER: US/11/212,443
| CURRENT FILING DATE: 1990-04-30
| PRIOR APPLICATION NUMBER: US/09/302,626
| PRIOR APPLICATION NUMBER: US/09/302,626
| PRIOR FILING DATE: 1999-01-14
| NUMBER OF SEQ ID NOS: 195
| SOFTWARE: Patentin Ver: 2.1
| SEQ ID NO 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Neisseria meningitidis
FEATURE:
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Best Local Similarity 32.7%;
Matches 18; Conservative
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OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: SITE
LOCATION: (30)
OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (232)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                US-11-212-443-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
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CUNTRY: United States of America

ZIP: 6060-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783

FILING DATE: 28-Jan-2003

CLASSIFICATION NUMBER: US/448,729

FILING DATE: 24-MAY-1995

APPLICATION NUMBER: 08/42,255

FILING DATE: 21-DEC-1933

APPLICATION NUMBER: 07/684,535

FILING DATE: 10-APR-1991

APPLICATION NUMBER: 07/59,71

FILING DATE: 10-APR-1991

APPLICATION NUMBER: 07/593,616

FILING DATE: 11-JUN-1990

APPLICATION NUMBER: 07/593,618

FILING DATE: 11-JUN-1990

APPLICATION NUMBER: 07/593,618
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S IAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCL 104
                                                                                                                                                                                                                                                                                                                              APPLICANT: Zsebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-10-353-783-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                      US-10-353-783-51; Sequence 51, Application US/10353783; Publication No. US20050261175A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 274 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312/474-0448
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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Best Local Similarity
Matches 26; Conserva
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Gaps

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; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR PILING DATE: 2004-07-20
; PRIOR FILING DATE: 2004-07-20
; PRIOR FILING DATE: 2004-07-20
; PRIOR FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PAREENTIN version 3.3
; SEQ ID NO 141
; LENGTH: 3716
; TYPE: PRI
CORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-141

Query Match
Best Local Similarity 35.0%; Pred. No. 2.5e+02;
Matches 14; Conservative 5; Mismatches 19; Indels 2; Gaps

QY
6 IAPTTDYRNTTATGLTSALN-LPQVHAFVNDWASLDMWW 43
; | | | | | | | | | | | |
Db 2445 VPPTPGRUTTATPSGFFNSGAGGVSGFGNVGSNLSGWW 2484

Search completed: January 18, 2006, 19:50:27
Job time: 9 secs
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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                                                                                                             ; Search time 70 Seconds
(without alignments)
1017.977 Million cell updates/sec
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                                                                                                                                                                                                                                  1 MTGSTIAPTTDYRNTTATGL......NEKIHRLDGLKPCSLLLQYD 101
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                     2166443 segs, 705528306 residues
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077928 ADE02
091023 ADE02
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QSC818_SCHJA
QSC807_SCHJA
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Maximum Match 100%
Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
                                                                                                                   January 18, 2006, 19:42:41
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
                                                                                                                                                                                           US-10-822-873-11
551
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Match Length DB
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Perfect score:
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11.6K protein.
Human adenovirus 2 (HAdV-2).
Viruses; debNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 551; DB 2; Length 101; 100.0%; Pred. No. 1e-52;
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                                                                                                                                                                                                                                                                                                                                                                        TISSUB=Ear swab, Respiratory epithelium, and Stool sample, Borcherding F., Pring-Akerblom P.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ2991915, CAG67721.1; -; Genomic_DNA.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR008652; Hum_adeno_E3A.
Pfam; PP05393; Hum_adeno_E3A; J.
SEQUENCE 101 AA; 11662 MW; 914F50AC2F8B284F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FB89FCC6E921E84B CRC64;
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                                                                                                           Last sequence update)
Last annotation update)
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Pred. No. 2.2e-52;
          101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AJ29314; CAC67713.1; -; Genomic_DNA.
EMBL, AJ293916; CAC67729.1; -; Genomic_DNA.
EMBL, AJ293917; CAC67737.1; -; Genomic_DNA.
EMBL, AJ293917; CAC67866.1; -; Genomic_DNA.
GO; GO:0016021; C:integral to membrane; IBA.
InterPro; IPR008665.2; Hum_adeno_E3A.
Efan; PFC5593; Hum_adeno_E3A.
EEQUENCE 101 AA; 11644 MW; FB89FCCGE921E
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          PRT;
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                                                                            Created)
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                                                                                                           10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                        10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                             11.6K protein.
Human adenovirus 2 (HAdV-2)
Q779E8 ADE02 PRELIMINARY;
Q779E8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q91023 ADE02 PRELIMINARY;
Q91023;
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Q91023
AC Q931
AC Q931
DDT 011-
DDT 011
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Reichmann H., Schaarschmidt E., Geieler B., Hausmann J., Ortmann D.,
Bauer U., Plunker G., Seidel W.;

Bauer U., Plunker G., Seidel W.;

"Sequence analysis of group C human adenoviruses type 1 and 6 for five
genes of region E3.";

Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Integral nuclear membrane protein.
-!- PTM: N-glycosylated and probably also O-glycosylated (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11.6K protein.
14.0k protein.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TAXID=10515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus
NCBI_TaxID=10534;
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14 14 N-linked (GlCNAC. .) (Potential).
101 AA; 11613 MW; EF219000939E3B4B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Borcherding F., Pring-Akerblom P.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ293913; CAC67704.1; -; Genomic_DNA.
GG, GO.016021; C.integral to membrane; IEA.
Interpro; IFR008652; Hum adeno_E3A.
Pfam; PF05393; Hum_adeno_E3A; I.
SEQUENCE 101 AA; 11704 MW; E13857DC5891E85B CRC64;
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99.0%; Pred. No. 4.8e-52;
tive 0; Mismatches 1;
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15-DEC-1998 (Rel. 37, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Early E3A 11.6 kDa glycoprotein.
Human adenovirus 6 (HAdV-6).
                              101 AA
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InterPro; IRR008652; Hum adeno E3A.
Pfam; PFC3939; Hum adeno E3A; I.
Early protein; Glycoprotein; Transmembrane.
TRANSWEM 41 62 Potential.
CARBOHYD 14 14 N'linked (GLCNY SEQUENCE 101 AA; 11613 MW; EF219000939E3
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r6_ADE02
Q$12J6_ADE02_PRELIMINARY;
Q912J6;
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TISSUE=Liver;
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NUCLEOTIDE SEQUENCE.
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                                                                                       NCBI_TaxID=28285;
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Q6VGT8_
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                                                                                                                 1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Hannover /Adrian German reference center for adenoviruses, seichmann H., Schaarschmidt E., Geisler B., Hausmann J., Ortmann D. Bauer U., Flunker G., Seidel W. Sedies W. Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human adenovirus 1 (HAdV-1).
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Hannover /Adrian German reference center for adenoviruses;
Reichmann H., Schaarschmidt E.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Natural variation among human adenoviruses: genome sequence and annotation of human adenovirus serotype 1.";
J. Gen. Virol. 85:2615-2625(2004).
EMBL; V11257; CAA72127.1; -; Genomic_DNA.
EMBL; V11032; CAA71216.1; -; Genomic_DNA.
EMBL; AF534906; AAQ10560.1; -; Genomic_DNA.
EMBL; AF534906; AAQ10560.1; -; Genomic_DNA.
EMBL; AF534906; AAQ10560.1; -; Genomic_DNA.
EMBL; PR05393; Hum adeno_E3A.
Franty PF05393; Hum adeno_E3A.
Franty PF05393; Hum adeno_E3A.
Franty PF05393; Hum adeno_E3A, Incorp.
Franty FF05393; Hum adeno_E3A, Incorp.
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PubMed=15302955; DOI=10.1099/vir.0.80118-0;
Lauer K.P., Llorente I., Blair E., Seto J., Krasnov V.,
Purkayastha A., Ditty S.E., Hadfield T.L., Buck C., Tibbetts C.,
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97.6%; Score 538; DB 1; Length 101; 98.0%; Pred. No. 2.8e-51; ive 0; Mismatches 2; Indels
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Pred. No. 3.8e-31;
8; Mismatches 9; Indels
                                                                                                                                                                                                                            61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                            61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLLQYD 101
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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Last annotation update)
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Name=Ad1/E3-11.6K;
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(Rel. 47, Last anno
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78.8%;
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                                                       99; Conservative
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE
                               Best Local Similarity
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01-AUG-1990
10-MAY-2005
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E311 ADEOS
ID E311 ADEOS
AC P17590;
DT 01-AUG-1990
DT 10-MAY-2005
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Query Match
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-22087470; PubMed=1727603; Chroboczek J., Bieber F., Jacrot B.; The sequence of the genome of adenovirus type 5 and its comparison with the genome of adenovirus type 2."; Virology 186:280-285(1992).
-- SUBCELLINGAR LOCATION: Integral nuclear membrane protein.
--- PTM: N-91ycosylated and probably also 0-91ycosylated.
--- SIMILARITY: Belongs to the adenoviruses B3A-1 family.
                                                                                                                                                                                                                                                                 adenovirus 5.";
Barly E3A 10.5 kDa glycoprotein.
Human adenovirus 5 (HAdV-5).
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=129951;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-linked (GlcNAc. . .) (Potential).
008AD087AAB45A8F CRC64;
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GO; GO:0016021; C:integral to membrane; IEA.
Interpro; IPRO08652; Hum_adeno_E3A.
Efam; PF05393; Hum_adeno_E3A; 1.
SEQUENCE 93 AA; 10523 WW; 008AD087AAB45A8F CRC64;
                                                                                                                                                                                       MEDIINE-85092388; PubMed=2981456;
Cladaras C., Wold W.S.M.;
"DNA sequence of the early E3 transcription unit of
Virology 140:28-43(1985).
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Last annotation update)
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EMBL; X03002; CAA26784.1; -; Genomic_DNA.
PIR; A05245; ERAD53.
InterPro; IPR008652; Hum_adeno_E3A.
Pfan; PF05393; Hum_adeno_E3A; I.
Early protein; Glycoprotein; Transmembrane.
TRANSMEM 34 55
                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA)
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QGVGT8;
05-JUL-2004 (TrEMBLrel. 27, 0
05-JUL-2004 (TrEMBLrel. 27, 1
05-JUL-2004 (TrEMBLrel. 27, 1
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NCBI_TaxID=10527;
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                                                                                                                             3 NITNAAAATGLISTINIPQVSAFVNNWDNLGMWWFSIALMFVCLIIMWLICCLKRKRARP
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PubMed=12560390; DOI=10.1136/jcp.56.2.120;
Adhikary A.K., Numaga J., Kaburaki T., Kawashima H., Araie M.,
Ikeda Y., Ogino T., Suzuki E., Ushijima H., Mukouyama A., Matsuno S.,
Inada T., Okabe N.;
Genetic Characterization of Adenovirus Type 8 Isolated in Hiroshima
                                                                                               14 NTT----ATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLICCLKRRRARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=8P prime;
PubMed=12560390; DOI=10.1136/jcp.56.2.120;
PubMed=12560390; DOI=10.1136/jcp.56.2.120;
Adhikary A.K., Numaga J., Kaburaki T., Kawashima H., Araie M.,
Ikeda Y., Ogino T., Suzuki E., Ushijima H., Mukouyama A., Matsuno S.,
Inada T., Okabe N.;
Inada T., Okabe N.;
Genetic Characterization of Adenovirus type 8 Isolated in Hiroshima
City over a 15-year Period.";
J. Clin. Pathol. 56:120-125(2003).
EMBL; ABI10079; BAC82700.1; -; Genomic DNA.
SEQUENCE 276 AA; 30879 MW; 838596E7F65BBEEE CRC64;
                                                       Gaps
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
5 protein adenovirus type 8E.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adenovirus 8 (HAdV-8).
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=31545;
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62.8%; Score 346; DB 2; Length 93; 78.3%; Pred. No. 3.7e-30; ive 6; Mismatches 8; Indels
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J. Glin. Pathol. 56:120-125 (2003).
EMBL; AB097769; BAC58004.1; -; Genomic DNA.
SEQUENCE 276 AA; 30919 MW; 587D4C95AE86BC26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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235 YFVCCKAREKSRRPIYRPVI 254
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Q76C86;
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Q80IV7;
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                                                    65; Conservative
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     Query Match
Best Local Similarity
Matches 65; Conserv
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                                                                                                                       9 TIDYRNTTATGLISALNLPQVHAFVND------WASLD--MWWFSIALMFVCLIIM 56
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PubMed=12560390; DOI=10.1136/jcp.56.2.120;
Adhikary A.K., Numaga J., Kaburaki T., Kawashima H., Araie M.,
Ikeda Y., Ogino T., Suzuki E., Ushijima H., Mukouyama A., Matsuno S.,
Inada T., Okabe N.;
"Genetic Characterization of Adenovirus type 8 Isolated in Hiroshima
                                                              13; Gaps
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=31545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ademovirus 9 (HAdV-9).
Viruses; dsDNA viruses, no RNA stage; Ademoviridae; Mastademovirus.
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18.6%; Score 102.5; DB 2; Length 296;
Best Local Similarity 26.2%; Pred. No. 0.0079;
Matches 21; Conservative 23; Mismatches 23; Indels 13;
      Length 276;
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                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Type strain: ATCC VR-1086;
Buettner W.H., Veres-Molnar S.K.;
"Adenovirus type 9, complete sequence.";
Submitred (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ854486; CALIOS981.1; -; Genomic DNA.
SEQUENCE 296 AA; 33125 WW; 256ED64914353439 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    City over a 15 year Period.";
J. Clin. Pathol. 56:120-125 (2003).
EMBL, AB106356; BAC87854.1; '20enomic DNA.
SEQUENCE 261 AA; 29415 MW; 91433010DAA306B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
E3 orf3 33.1 kba protein.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Query Match
19.5%; Score 107.5; DB 2;
Best Local Similarity 28.8%; Pred. No. 0.0021;
Matches 23; Conservative 21; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 AA
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255 YFVCCKAREKSRRPIYRPVI 274
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Q76ELS;
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QSTIZ2;
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completed: January 18, 2006, 19:47:55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
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Job time : 73 secs
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Q90770 CHI
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                                                                                 TGSTIAPTTDYRNTTATGLTSALNLPOVHAFVNDWASLDMWWFSIALMFVCLIIMWLICC
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PubMed=12560390; DOI=10.1136/jcp.56.2.120;
Adhikary A.K., Numaga J., Kaburaki T., Kawashima H., Araie M.,
Ikeda Y., Ogino T., Suzuki E., Ushijima H., Mukouyama A., Matsuno S.,
Inada T., Okabe N.;
"Genetic Characterization of Adenovirus Type 8 Isolated in Hiroshima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adenovirus type 46.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=31545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 18.2%; Score 100.5; DB 2; Length 281; Local Similarity 26.2%; Pred. No. 0.012; les 21; Conservative 22; Mismatches 24; Indels 13;
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16.4%; Score 90.5; DB 2; Length 259;
Best Local Similarity 22.5%; Pred. No. 0.14;
Matches 18; Conservative 23; Mismatches 26; Indels 1:
                                 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome Sequence of Human adenovirus type 46.";
Submitted (DRC-2004) to the EMBL/Genbank/DDBJ databases.
EMBL; AY875648 AX770339.1; -; Genomic DNA.
SEQUENCE 281 AA; 30918 MW; 23CF181230DA2032 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                City over a 15-year Period.";
J. Clin. Pathol. 56:120-125(2003).
EMBL; AB102672; BAC78834.1; -; Genomic DNA.
SEQUENCE 259 AA; 29138 MW; D3742E9ADBAC5CF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                       281 AA
       Pred. No. 0.01;
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24.0%; Preα. ας.
tive 23; Mismatches
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225 KARKKSRRPIYRPVI 239
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                                                                                                                                                                               62 LKRRRARPPIYRPII 76
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Q4KS19 9ADEN PRELIMINARY;
Q4KS19;
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Q7TBG9;
                                 18; Conservative
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     Best Local Similarity
Matches 18; Conserv
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O77E69 ADE
O77E69
D7 01-0C

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141 TTAAPTTAAATTQSSHVNKDICMPSSEPGTSSENILNLYCEIFIWAPL----AGVCLVLL 196
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                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CD8 alpha chain precursor.
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tregaskes C.A., Kong F.K., Paramithiotis E., Chen C.1.H., Ratcliffe M.J.H., Davison T.F., Young J.R.;
Ratcliffe M.J.H., Davison T.F., Young J.R.;
"Identification and analysis of the expression of CD8 alpha beta and CD8 alpha alpha isoforms in chickens reveals a major TCR-gamma delta CD8 alpha beta subset of intestinal intraepithelial lymphocytes.";
J. Immunol. 154:4485-4494 (1995).
EMBL, Z22726; CAA80421.1; -; mRNA.
BIR; ISO610; ISO610.
Ensembl; ENSGALGO000015816; Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 14.0%; Score 77; DB 2; Length 235; 1 Similarity 25.2%; Pred. No. 4; 26; Conservative 18; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 CLIIMWLICCLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPC 94
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26100 MW; 525326EE1AA4B512 CRC64;
                                                                                                                                                                                                                                                                                                                           235 AA
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                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                      218 YFVCCKTKKKSRRPIYRPVI 237
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                                                                                                  92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
Pfam; PP00047; ig; I.
SMART; SM00409; IG; I.
IMPOSTITE; PS50835; IG_LIKE; I.
Immunoglobulin domain; Signal.
SIGNAL
                                                                                                  57 WLICCLKRRRARPPIYRPII
                                                                                                                                                                                                                                                                                                                        Q90770_CHICK PRELIMINARY;
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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OM protein - protein search, using sw model

January 18, 2006, 19:43:21 Run on:

, Search time 16 Seconds (without alignments) 607.368 Million cell updates/sec

Title:

US-10-822-873-11 551 1 MTGSTIAPTTDYRNTTATGL.....NEKIHRLDGLKPCSLLLQYD 101 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	early E3A 10.5K or	Burface o	disintegrin (EC 3.	NADH2 dehydrogenas	epoxide hydrolase	disintegrin (EC 3.	hypothetical prote	_	hypothetical prote	~	_	=	transmembrane glyc	hypothetical prote	hypothetical prote			hypothetical prote	copper resistance	hypothetical prote	protein-tyrosine k	protein-tyrosine k	multidrug-efflux t	probable membrane	protein F21D18.14	hypothetical prote	U	hypothetical prote	
SUMMARIES	ERAD53	150610	S52477	850336	T01316	866129	872597	AG0784	AH2409	T28767	T19413	S52920	A46103	T19416	T48284	T22046	T19412	S42125	S52258	T22922	I48696	148697	G69804	T36483	E96521	F87652	T14339	H82690	T15863
DB	-	~			~																					~			8
Length	66	235	544	316	324	748	95	518	429	340	1187	491	522	533	428	244	306	279	466	242	871	881	518	83	150	254	501	638	1667
& Query Match	62.8	14.0	13.4	13.1	12.7		12.6	12.6	12.3	12.3	12.3	12.2	12.2	12.2	12.1	12.0	11.9	11.8	11.8	11.7	11.7	11.7	11.6	11.5	11.5	11.5	11.5	11.5	11.5
Score	346	77	74	72	70	70	•	69.5	68	67.5	•	67	67	67	66.5	99	65.5	65	65	64.5	64.5	64.5	64	ë.	63.5	ë.	63.5	63.5	63.5
Result No.	-	101	m	4	2	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Score 77; DB 2; Length 235; Pred. No. 0.55;

14.0%; 25.2%;

Query Match Best Local Similarity

UL73 glycoprotein large surface anti SSUI protein - yea hypothetical prote hypothetical prote protein W06E11.6 [probable membrane TRK potassium upta hypothetical prote hypothetical prote exopolyaaccharide E1 membrane glycop hypothetical prote mating-type mating-type mating-type b3 protein - smut	protein T6D22.10 [
QQBEB2 S67506 S7506 S71974 S701974 T00529 T00529 E88382 E883324 E8433 AH1148 AH148 AH1	B86215
	N
133 445 462 333 444 100 100 100 100 100 100 100	603
11111111111111111111111111111111111111	11.2
622 623 625 625 627 627 627 627 627 627 627 627 627 627	61.5
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# ALIGNMENTS

· · · · · · · · · · · · · · · · · · ·	RESULT 1 ERAD53 early E3A 10.5K protein - human adenovirus 5 c;Species: Mastadenovirus h5 (human adenovirus 5) C;Species: Mastadenovirus h5 (human adenovirus 5) A;Note: host Homo sapiens (man) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004 C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004 C;Accession: A05245 R;Cladaras, C.; Wold, W.S.M. Virology 140, 28-43, 1985 A;Accession: A05245 C;Superfamily: adenovirus early E3A 10.5K protein C;Superfamily: adenovirus early E3A 10.5K protein C;Keywords: early protein; transmembrane protein	1-2004 3 5. NID:958503; PIDN:C
	Query Match 62.8%; Score 346; DB 1; Length 93; Best Local Similarity 78.3%; Pred. No. 6.2e-31; Matches 65; Conservative 6; Mismatches 8; Indels 4; C	Gaps 1;
	Qy 14 NTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMMLICCLKRRRARP	RARP 69       RARP 62
	Oy 70 PIYRPIIVLAPHNEKIHRLDGLK 92	
	RESULT 2 150610 T-cell surface glycoprotein CD8 alpha chain - chicken C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004 C;Accession: 150610; 833350 C;Accession: 150610; 833350 R;Tregaskes, C.A.; Kong, F.K.; Paramithiotis, E.; Chen, C.L.; Ratcliffe, M.J.; Davison, J. Immunol. 154, 4485-4494, 1995 A;Title: Identification and analysis of the expression of CD8 alpha beta and CD8 alpha ymphocytes. A;Reference number: 150609; MUID:95238946; PMID:7722305 A;Accession: 150610 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-235 <tre> A;Residues: 1-235 <tre> A;Cross-references: UNIPROT:Q90770; UNIPARC:UP100000FBABF; EMBL:Z22726; NID:g488149; PI C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: glycoprotein</tre></tre>	ie, M.J.; Davison, sta and CD8 alpha a ;, NID:g488149; PIDb

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A,Molecule type: DNA
A,Residues: 1.-324 «KAL»
A,Cross-references: UNIRROT:081299; UNIPARC:UPI00000AC70B; EMBL:AF069298; NID:g3193282; E.
A,Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disintegrin (EC 3.4.24.-) precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-401-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S66129; 32205
R;Glynn, P.; Howard, L.
R;Glynn, P.; Howard, L.
R;Glynn, P.; Howard, L.
A;Description: identification of a mammalian member of the metalloproteinase/disintegrin
A;Reference number: S66129
A;Accession: S66129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-748 <GLY>
A;Cross-references: UNIPROT:Q10741; UNIPARC:UP100001254C7; EMBL:Z21961; NID:g1044810; PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, March 1993
A;Description: Identification of a mammalian member of the metalloproteinase/disintegrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;;
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                                                                                                                                                                                                                                                                                                                                         epoxide hydrolase homolog T14P8.15 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 GLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLICCLKRRRARPPIYRPIIVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, MOLECULE type: MRNA
A, Residues: 1-113, 'LAM', 117, 'LLLMEDLKDSFRLMVAR', 135-171, 'R', 173-652, 'L',
A, Residues: 1-113, 'LAM', 117, 'LLLMEDLKDSFRLMVAR', 135-171, 'R', 173-652, 'L',
A, Cross-references: UNIPARC: UNIONO174F9; EMBL: 221961
A, Note: this sequence Har revised in reference S66129
C; Keywords: hydrolase; metalloproteinase; zinc
F; 1-13/Domain: signal sequence #status predicted <SIG>
F; 14-748/Product: metalloproteinase #status predicted <MAT>
F; 456-546/Domain: disintegrin homology <DIS>
F; 383, 387, 393/Binding site: zinc, catalytic (His) #status predicted
F; 384/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Note: this is a revision to the sequence from reference S32205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Accession: T01316
R;Kalicki, J.; Elliott, G.; Cloud, J.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of A. thaliana T14P8.
A;Reference number: 214290
A;Accession: T01316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.7%; Score 70; DB 2
Best Local Similarity 20.3%; Pred. No. 4.4;
Matches 15; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 GLLDSLGVDRVFLVGHDWGAIVAWW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJ
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23.7%;
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|29 NPRNPSVKPVDAFR 142
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                                                               :: ||
188 IVVCLAETNRAP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 4
A;Introns: 155/3; 235/2
A;Note: T14PB.15
C;Superfamily: tropinesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: S32205
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S544', distributed (EC 3.4.24.-) precursor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 08-May-1995 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C;Accesion: 552477
R;HOward, L.; Mitchell, S.; Lu, X.; Griffiths, S.; Glynn, P.
R;HOward, L.; Mitchell, S.; Lu, X.; Griffiths, S.; Glynn, P.
R;HOward, L.; Mitchell, S.; Lu, X.; Griffiths, S.; Glynn, P.
R;HOward, L.; Mitchell, S.; Lu, X.; Griffiths, S.; Glynn, P.
A;Reference number: 552477
A;Reference number: 552477
A;Accession: 67247
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C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C; Accession: S50336
R; Boore, J.L.; Brown, W.M.
Genetics 138, 423-443, 1994
A; Title: Complete DNA sequence of the mitochondrial genome of the black chiton, Katharin A; A; Reference number: S50327; MUID:95129806; PMID:7828825
A; Molecule type: DNA
A; Residues: 1-316 <BOO>
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A;Gene: ND1
A;Gene: mitochondrion
A;Genetic code: SGC4
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                          | | | | : | : : : | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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     Gaps
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26;
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18; Mismatches 33; Indels
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                                                                                                     4 STIAPTTDYRNTTATGL-
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     26; Conservative
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Best Local S:
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셤 ઠે 셤

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Clacesion: T28767
Ripoliting, T.; Wohldmann, P.
Biboliting, T.; Wohldmann, P.
Albescription: The sequence of C. elegans cosmid W03D2.
Albescription: T28767
Albescription: T2876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q8YMU5; UNIPARC:UPI0000CEC7A; GB:BA000019; PIDN:BAB76531.1; A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 GLVEVLTLPERVIHASGASVYLFVDSFLRYEKWIANPLAALYACSFALCITLL----AS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein W03D2.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C23H4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19413
R;Wilkinson, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 TWFKQWVAVDLIWAIAAALIMGFVVAKAIVWIDQKVQKRRSADALMEDFIALS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 AFVNDWASLDMWWFSIALMF----VCLIIMWLICCLKRRARPPIYRPIIVLN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.3%; Score 67.5; DB 2; Length 340; Best Local Similarity 25.0%; Pred. No. 8.7; Matches 21; Conservative 16; Mismatches 30; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MTGSTIAPT-----TDYRN-----TTATGLTSALNLPQVH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 12.3%; Score 68; DB 2; Length 429; Similarity 21.2%; Pred. No. 9.8; 24; Conservative 19; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 4
A;Introns: 63/3; 118/2; 185/3; 210/3; 253/3; 314/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 HFVFRYIAVCRPHD--LHHLEGWK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 PPIYRPIIVLNPHNEKIHRLDGLK 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-429 <KUR>
                                                                                                                                                                                                                                                                                                                                                  A; Accession: AH2409
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                              A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: UNIPARC:UP10000059BBE; GB:AL513382; PIDN:CAD02597.1; PID:g16503453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                         678
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                                                                      ----TTATG----LTSALNLPQVHAFVNDWASLDMWW 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 TIA--PITDYRNTTATGLISALNLPQVHAFVNDWASLDMWWFSIALMFVCL--IIMWLIC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein B1937 F2_47 - Mycobacterium leprae
C;Species: S;Ss97
R;Smith, D.R.; Robison, K.
Submitted to the EMBL Data Library, November 1993
A;Reference number: S72580
A;Reference number: S72580
A;Reference number: S72597
                                                                                                                Gaps
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                                                                                                                                                                                                                                                   74
                                                                                                                                                                                                            --- CLKRRRARPPIYRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 TIDYRNTTATGLISALNIPQVHAFVNDWASLDMWWFSIALMFVCLIIM 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.6%; Score 69.5; DB 2; Length 95; 29.2%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27; Indels
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       26; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 YFIYALRTRPGKEILTAIKHEQFYVVYQPVV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----PIYRPII 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Mismatches
       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: probable membrane protein ylaB
       17;
                                                                      3 GSTI----APTTDYRN----
                                                                                                                                                                                                         44 FSIALMFVCLIIMWL----IC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.6%;
26.4%;
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   27; Conservative
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A; Residues: 1-518 < PAR>
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       Matches
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C;Accession: A46103; D46104
R;Tordo, N.; Bourhy, H.; Sather, S.; Ollo, R.
Virology 194, 59-69, 1993
A;Title: Structure and expression in baculovirus of the Mokola virus glycoprotein: an eff.
A;Reference number: A46103; MUID:93242783; PMID:8480429
                                                                                                                                                                                                                                        A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-522 < TOR>
A;Residues: 1-522 < TOR>
A;Cross-references: UNIPROT: 089507; UNIPARC: UPI00000F7438; GB: S59447; NID: 9299713; PIDN: J;
A;Note: sequence extracted from NCBI backbone (NCBIN: 130538, NCBIP: 130541)
R;Bourhy, H; Kissi, B; Tordo, N.
A;Rology 194, 70-81, 1993
A;Title: Molecular diversity of the Lyssavirus genus.
A;Caference number: A46104; MUID: 93242784; PMID: 8386891
A;Cottents: lyssavirus serotype 3
A;Accession: D46104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: genomic RNA
A;Residues: 1-522 <BOUS
A;Coss-references: UNIPARC:UPIO0000F7438; GB:S59448; NID:g299715; PIDN:AAB26296.1; PID:g1
A;Coss-references: UNIPARC:UPIO000F7438; GB:S59448; NID:g299715; PIDN:AAB26296.1; PID:g1
A;Note: sequence extracted from NCBI backbone (NCBIN:130542, NCBIP:130548)
C;Superfamily: rabies virus spike glycoprotein
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A;Cross-references: UNIPARC:UP1000007A484; EMBL:269717; PIDN:CAA93533.1; GSFDB:GN00028; </
A;Experimental source: clone E01G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 14/1; 54/1; 58/3; 125/3; 162/1; 194/1; 234/1; 295/1; 319/1; 354/2; 403/1; 455/
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A;Molecule type: DNA
A;Cross-references: UNIPROT:017592; UNIPARC:UPI000007A484; EMBL:Z78416; PIDN:CAB01683.1;
A;Experimental source: clone C2344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTGSTIAPTTDYRNTTATGLT-----SALNLPQVHAFVNDWASLDM---WWFSIALMFV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein E01GG.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19416; T20408
C;Date: 07-Apr-1994 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
12.2%; Score 67; DB 2; Length 522;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 17; Conservative 9; Mismatches 19; Indels
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submitted to the EMBL Data Library, August 1996
A;Reference number: Z19121
A;Accession: T19416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 30.1%
Matches 22; Conservative
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A;Accession: T20408
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distributed (EC 3.4.24.-) - human (fragment)
c;Species: Homo sapiens (man)
c;Species: Homo sapiens (man)
c;Species: Homo sapiens (man)
c;Species: O6-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 15-Mar-2004
c;Accession: S52920; PC4265
R;Howard, L.; Lu, X.; Mitchell, S.; Griffiths, S.; Glynn, P.
submitted to the EMBL Data Library, March 1995
A;Pescription: Molecular cloning of MADM: a catalytically active mammalian disintegrin-mananer: S52920
A;Accession: S52920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: PC4265
A,Status: nucleic acid sequence not shown
A,Molecule type: mRNA
A,Moslecule type: mRNA
A,Resdiues: 1-247 <MCKA
A,Resdiues: 1-247 <MCKA
A,Experimental source: articular chondrocyte
C,Comment: This protein is a membrane bound protein and involved in cell/cell and cell/m
C,Keywords: hydrolase; metalloproteinase
F,126-136/Domain: metal-binding #status predicted <MEB>
F,126-136/Domain: disintegrin homology <DIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPARC:UPI0000150908; EMBL:Z48579
R;McKie, N.; Edwards, T.; Dallas, D.J.; Houghton, A.; Stringer, B.; Graham, R.; Russell,, Biochem. Bloophys. Res. Commun. 230, 333-339, 1997
A;Title: Expression of members of a novel membrane linked metalloproteinase family (ADAM A;Reference number: PC4263; MUID:97168971; PMID:9016778
                                                        A;Accession: T19413
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1187 <WIL>
A;Cross-references: UNIPROT:Q93254; UNIPARC:UPI000017B7AA; EMBL:Z78416; PIDN:CAB01680.1;
A;Experimental source: clone C23H4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                     A;Map position: X
A;Introns: 48/3; 81/2; 114/3; 182/1; 278/3; 346/3; 401/1; 486/1; 538/3; 635/3; 668/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGSTI-----APTTDYRN-----TTATG----LTSALNLPQVHAFVNDWASLDMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 STIAP--TIDYRNTTATGLISALNIPQV-----HAFVNDWASLDMWWFSIALMFVCLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.3%; Score 67.5; DB 2; Length 1187; Best Local Similarity 22.4%; Pred. No. 31; Matches 19; Conservative 15; Mismatches 34; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.2%; Score 67; DB 2; Length 491; Best Local Similarity 23.5%; Pred. No. 14; Matches 27; Conservative 17; Mismatches 27; Indels
              submitted to the EMBL Data Library, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WFSIALMFVCLIIMWL----IC-----
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C;Species: Mokola virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SS IMMLICCLKRRR-----ARPPI 71
                                             A; Reference number: Z19121
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A.Molecule type: mRNA
A.Residues: 1-491 <HOW>
                                                                                                                                                                                                                                                                                                                     A, Gene: CESP: C23H4.3
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Gaps

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RESULT 15
T48284
T48284
Typethetical protein T22P11.220 - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C.Accession: T48284
R.Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, April 2000
A,Reference number: Z24490
A,Reference number: Z24490
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-428 <BEV>
A,Residues: 1-428 <BEV>
A,Residues: 1-428 <BEV>
A,Residues: 1-428 <BEV>
Cross-references: UNIPROT:Q9L239; UNIPARC:UP1000000C613; EMBL:AL162971
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.1%; Score 66.5; DB 2; Length 428;
Best Local Similarity 25.0%; Pred. No. 14;
Matches 15; Conservative 11; Mismatches 21; Indels 13; Gaps
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A; Note: T22P11.220
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Search completed: January 18, 2006, 19:48:21 Job time : 18 secs

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e version 5.1.6	- 2006	
GenCore	(c) 1993	
	Copyright	

OM nucleic - nucleic search, using sw model	January 20, 2006, 19:01:31; Search time 3753 Seconds (without alignments) 3827.241 Million cell updates/sec
OM nucleic - nucl	Run on:

	(Without allyments) 3827.241 Million cell updates/
Title: Perfect score:	US-10-822-873-10 307
Sequence:	1 gatgaccggctcaaccatcgttcttttacagtatgattaa 307

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched: 41078325 segs, 23393541228 residues

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

82156650

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

EST:*

1: qb_est1:*
2: qb_est2:*
3: qb_est3:*
4: qb_est3:*
5: qb_est4:*
6: qb_est5:*
7: qb_est6:*
8: qb_est7:*
9: qb_qss1:*
10: qb_qss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	CD364758	756 BU777756 SJEDNF08	879 BF272879 GA Eb001	DT112306	495 AW187495 BNLGHi587	_	C0116311 GR			163 BZ997163 PUGFJ11TD			2662 CG882662 ZMMBBb049			172 CV949172 PVrpvb 13		0781 CL990781 ZMMBHF000	TA303D04P AL497488 T. brucei	271 BMBAC347H	BX757054	066 PVrnvh 47
	£	CD364758	BU777756	BF272879	DT112306	AW187495	CO122313	CO116313	AG974323	CV926	BZ997163	CG401905	CC401331	CG882662	BX214284	CZ95	CV949172	CV959926	CL990781	TA30	BH76727	BX757054	CV951066
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de	Query Match	63.8	13.2	13.0	12.6	12.5	12.5	12.5	12.4	12.2	12.0	12.0	12.0	12.0	11.9	11.9	11.8	11.8	11.8	11.7	11.7	11.7	11.6
	Score	196	40.6	40	38.8	38.4	38.4	38.4	38.2	37.6	36.8	36.8	36.8	36.8	36.4	36.4	36.2	36.2	36.2	36	36	35.8	35.6
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	EXISSE41 DANIO FER CV907775 PDRPCG 27 CD845789 DHOABOOGE AIS73060 tr69a09.x			BH733089 BOMBF75TR CE614912 tigr-gss- CV906572 PDTpcd 14 BX269320 BX269320	AG536301 Mus muscu CK160091 FCAS04163 CF68535 CCACU16TR AA051869 CN0055-5
	CV907775 CD845789 AI573060	BZ899030 CX602294 BH261969		BH733089 CE614912 CV906572 BX269320	AG536301 CK160091 CF685536 AA051869
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35.6 35.6	35.4 35.2 35.2	35 35 34.8	33333 4444 5444 5666 6644	4.2.2.2	34 . 2 34 . 34 34 . 34
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## ALIGNMENTS

CD364758 T39 bp mRNA linear EST 05-AUG-2004 UI-H-FT2-bjm-j-05-0-UI.sl NOI CGAP_FT2 Homo sapiens CDNA clone UI-H-FT2-bjm-j-05-0-UI 3', mRNA sequence. CD364758 CD364758 I GI:31148848 EST. Homo sapiens (human)	nuclidate; nucconstructions of the property of the property of the page of the property of the page of the property of the produce of the property preparation: Dr. M. Bento Soares, University of I contary preparation: Dr. M. Bento Soares, University of I contary preparation: Dr. M. Bento Soares, University of I contary preparation: Dr. M. Bento Soares, University of I contary preparation: Dr. M. Bento Soares, University of I contary Sequencing by: Dr. M. Bento Soares, University of I contary Sequencing by: Dr. M. Bento Soares, University of I contartion: Distribution information can be found at thtp://genome.ulowa.edu/distribution/cgap.html Seq primer: M13 FORWARD POLYA-YES.	Location/Qualifiers  1.739  / Organism="Homo sapiens" / Organism="Homo sapiens" / Ab_xref="taxon:9606" / Ab_xref="taxon:9606" / Clone="UI-H-FT2-bjm-j-05-0-UI" / tissue_type="Alveolar Macrophage" / des_tasge="Adult" / lab_host="NGI_CGAP_FT2" / clone=lib="NGI_CGAP_FT2" / clone=lib="NGI_CGAP_FT2" / clone=lib="NGI_CGAP_FT2" / clone=lib="NGI_CGAP_FT2" / clone=lib="NGI_CGAP_FT2" / clone lib="NGI_CGAP_FT2" / clone lib="nGI_CGAP_F
RESULT 1 CD364758/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES BOUTCE

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the conditions, other donor macrophages in different conditions, other donor macrophages in different conditions, other donor macrophages in different construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Klebsiella aureus moi 10, 24 hours; Klebsiella aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (AdS CMV eGFP), moi 500, 3 hours; Adenoviral vector (AdS CMV eGFP), moi 500, 3 hours; wt adenovirus moi 500, 3 hours; Adenovirus moi 500, 3 hours; Adenovirus moi 500, 24 hours; wt adenovirus and 500, 3 hours; Adenovirus moi 500, 24 hours; wt adenovirus and 500, 3 hours; Advector + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 4 hours;
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Schistosoma japonicum
Schistosoma japonicum
Bukaryota; Metazoa Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosoma.

1 (bases 1 to 390)
Hu,W, Yan,O., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R.,
Wang,Z.J., Rong,Y.P., Zen,L.C., Wu,J., Zhang,X., Wang,J.J.,
Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
McManus,D.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G.
Evolutionary and blomedical implications of a Schistosoma japonicum
Complementary DNA resource
Omplementary DNA resource
Nat. Genet. 35 (2), 139-147 (2003)
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
some normal donor macrophages were cultured in some of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCATTGTGCTCAACCCACACAATGAAAATTCATAGATTGGACGGTCTGAAAC-CATGT
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SJEDNF08 SJE Schistosoma japonicum CDNA, mRNA sequence.
BU777756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Iowa.
TAG_IISSUE-Human Lung Alveolar Macrophage
TAG_LIB-UI-H-FT2
TAG_SEQ-6GGCCATGCCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.8%; Score 196; DB 6;
86.4%; Pred. No. 1.2e-50;
iive 0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 TCTCTTCTTTACAGTATGATTAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rcrrrrcrrracagrargarraa 44
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossyptum.
1 (bases 1 to 533)
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J.,
Ming, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J.,
An integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
On Nov 17, 2000 this sequence version replaced gi:11203949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF272879
GA_Eb0016C17f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum p-10 dpa fiber library Gossypium arboreum penance.
                                                                                                                                                                                                                                                                                                                                      192
                                                                                                                                                                                                                                                                                                                                                                              193 CAGACGCCCCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCCACAATGAAAA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 grcaaaacacagarcacrcagrrarcrgargaggarcarrcrgggaaraarrcagagaa 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:29729"
/clone="GA__Bb0016C17f"
_tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_l: EcoRI; Site_2: Xhol"
                                                                                                                                                                                                                                                                                                                                      133 ITCCATAGCGCTTATGTTTGCCTTATTATTATGTGGCTTATTTGTTGCCTAAAGCG
                                                                                                                                                                                                                                                                                                 Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 AATTTATGATCTGCCGGATATGAACCAATGTTTTTTAGTTTTCCAGT 161
                                                                                                                                                                                                                                                  DB 5; Length 390;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                        161
               Location/Qualifiers
1. 390
/organism="Schistosoma japonicum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .533
/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                  Score 40.6; DB Pred. No. 0.18; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University Genomics Institute
                                                                               /mol_type="mRNA"
/db_xref="taxon:6182"
/tissue_type="Whole egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                             /dev_stage="egg"
/lab_host="rabbits"
/clone_lib="SJE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="8400"
Email: hanzg@chgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF272879.2 GI:13247883
                                                                                                                                                                                                                                                       Query Match
13.2%;
Best Local Similarity 52.7%;
Matches 88; Conservative
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BF272879
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selected using 1% agarose gel electrophoresis. (L \sim0.5-1.2k, M \sim1.2-2.5k, H \sim2.5k) and then inserted into the vector using site specific recombination (flanking attB sites on CDNA). The work was done at DOB Joint Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW187495 ST3 bp mRNA linear EST 30-NOV-1999
BNLGHi5871 Six-day Cotton fiber Gossypium hirsutum cDNA 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gossypium hirsutum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 573)
Blewitt,M., Matz,B.C. and Burr,B.
Graf Gossypium (developing cotton fiber (1999b)
Contact: Ben Burr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 IGTCAATGACTGGGCGAGCTTGGACATGTGGTGGTTTTTCCATAGCGCTTATGTTTTG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 TTTCTATTAGGAGGCTGGCTTTTAACAGGTGAAGCCAGTGAAAAGTGTTTGCATTTGTGGG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423 AATTGCTGGAATGTTCCATATGCGATCCACGAGTTCAGCCTGGACCCCCACTTA 482
                                                                                                                                                                                                                                                                        158 GTCGATGTCAGGCCTTGACTGGACATGTAGTTTTCCTTTCCTTTCCATTTTGTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 CCTTATTATTATGTGGCTTATTTGTTGCCTAAAGCGCAGACGCGCCAGACCCCCCCATCTA
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                                                                                                                                                                          8; Length 648;
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/lab_host="XL1-Blue"
/clone lib="Six-day C"
/note="Vector: pBluescript II KS+"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                     0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.5%; Score 38.4; DB 1;
llarity 55.1%; Pred. No. 0.95;
Conservative 0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 573
/organism="Gossypium hirsutum"
/mol_type="mRNA"
/culTivar="Acala Maxxa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:3635"
/tissue_type="immature fiber"
                                                                                                                                                                          Score 38.8; DB
Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                      158 CTTATTATTATGTGGCTTATTTGTTGCCTA 187
                                                                                                                                                                                                                                                                                                                                                                                                  98 CITALTALATGLACIGLITIGLITAALA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gossypium hirsutum (upland cotton)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
Email: burr@bluxl.bnl.gov
Seq primer: T3 Primer.
Location/Qualifiers
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AWI87495.1 GI:6461931
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                                                                                                                                                                          12.6%;
64.4%;
                                                                                                     Institute."
                                                                                                                                                                     Query Match
Best Local Similarity 64.4:
Matches 58; Conservative
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Best Local Similarity
Matches 75; Conserv
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AW187495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cdna@jgi_psf.org

Email: cdna@jgi_psf.org

CDNA Library Preparation: DOE Joint Genome Institute:

http://www.jgi.doe.gov

DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov

Naming Conventions: EST name is generated by the concatenation of

the JGI Clone Id and the direction of sequencing. The suffix 'rev'

indicates a reverse sequencing read of the insert. It does not

necessarily reflect the orientation of the insert. It does not

Poly.A. Based upon the presence of a run of 14 or more T residues

at the beginning of the sequence, this clone was polyadenylated.

The resulting Poly-T sequence has been removed.

Plates ANNO 0021 row: a column: 5

High quality sequence stop: 553

POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OGI_ANNO1937.rev ANNO Pimephales promelas Whole (M) Pimephales promelas CDNA clone ANNO1937 3', mRNA sequence.
                                                     ö
                                                                                                                                                                                                 216
                                                                                                                                           TTTCTATTAAGAGGCTGGCTTTAACAGGTGAAGCCAGTGAAGAGTGTTTGCCATTTGTGGG 141
                                                                                                                                                                                                                                            142 AATTGCTGGAATGTTCCATATGCGATCCACGAGTCGGAGTTCAGCCTGAACCCCCACTTA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pimephales promelas
Pimephales promelas
Rudaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Pimephales.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pDONR222; The library was made from dr
primed cDNA and cloned into Invitrogen vector pDONR222.
Poly A RNA were primed with a Biotin-attB2-01igo(dT)
primer (5'- GGCGGCGGACAACTTTGTACAAGAAAGTTGGGT(T)19 -3')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and the first strand synthesized using Superscript II (Invitrogen). The second strand was synthesized and an attBl adaptor was ligated to the 5' end (5' - regregescaractristancharhadatres - 3' and 5' -
                                                                                                                                                                                            157 CCTTATTATTATGTGGCTTATTTGTTGCCTAAAGCGCAGACGCCCAGACCCCCCATCTA
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAACTITITIGIACAAAGITGICCCC -3') . The cDNA was size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 648)
Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Broketein, P. and Lindquist, E.A.
DOE Joint Genome Institute Pimephales promelas EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Whole"
/dev_stage="Adult"
/clone_lib="ANNO Pimephales promelas Whole (M)"
                                                     ö
Score 40; DB 2; Length 533;
Pred. No. 0.29;
0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Pimephales promelas"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2005)
Other ESTs: JGI ANNO1937.fwd
Contact: Lindquist,E.A., Richardson,P.
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                                                                                                                                                                                                                                                                                          217 TAGGCCTATCATTGTG 232
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  13.0%;
55.9%;
                                                  76; Conservative
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Query Match
Best Local Similarity
Matches 76; Conserv
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Gaps

216

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Submitted (19-JAN-2005) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS 01-FEB-2005
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium. I bases 1 to 86. Kim, H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 TTTCTATTAGGAGGCTGGCTTTAACAGGTGAAGCCAGTGAAGAGTGTTTGCGTGTTTGTGGG 296
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Toshio,T.K. and Sakaki,Y.
BAC end sequences of Library DNB1
Unpublished
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                                                                                                                                                                                       Global assembly of Cotton ESTs
Unpublished (2004)
Unpublished (2004)
Contact: Ming
Arizona Genomics Institute
The University of Arizona
The University of Arizona
The University of Arizona
Tel: 520 626 9595
Fax: 520 626 9595
Email: rwing@gene.arizona.edu
Plate: 018 row: I column: 06.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Gossypium raimondii"
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Drosophila simulans DNA,
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                                                                                                                                       22313 856 bp mRNA linear EST 16-JUN-2004
Eb03001.f GR_Eb Gossypium raimondii cDNA clone GR_Eb03001 5',
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GOSSYPJUM raimondii
GOSSYPJUM raimondii
Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
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Gossypium raimondii
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev stage="3 to +3 DPA"
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ECORV; Library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 856)
Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Wdall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and Wing,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Global assembly of Cotton ESTs
Uppublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Porbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwingegenome.arizona.edu
Plate: 03 row: O column: 01.
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CO116311.1 GI:48814998
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ilarity 55.1%;
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Matches 75; Conservat
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                                                                          RESULT 6
CO122313
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754 bp DNA linear GSS 25-MAR-2003 PUGFJIITD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa371B22, genomic survey sequence.
BZ997163.1 GI:29240580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 TTTTTTTTAATGAGGACAGTCATGTCTCCACATGTATATTCCCATTATTGTTTCGCA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 754)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
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COT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 GGACATGTGGTGGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATTATGTGGCTTAT
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                                                                                                                                                                                                                                                                                                                                        12.2%; Score 37.6; DB 8; Length 598; 54.3%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                        64; Indels
                               1. .598
/organism="Phytophthora infestans"
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                                                                                                                                                                                                                  /clone lib="sporangia, purified"
/note="Vector: psPORT1"
                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                         /db_xref="taxon:4787"
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Class: sheared ends.
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      Location/Qualifiers
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Other GSSs: PUGFJIITB
Contact: Cathy Whitelaw
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Best Local Similarity 54.3'
Matches 76; Conservative
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Phytophthora.

1 (bases I. Dec.)

2 (bases I. Dec.)

3 (bases I. Dec.)

4 (bases I. De
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                                                                                                                  (yamamoto@kit.jp).
Submitted (30-11-2004) by Maaahira Hattori,
RIKEN, Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp,Tel:81-45-503-9111,
This work was done in collaboration with Yamamoto, M-T. Drosophila Genetic Resource Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 ATAGGCCTATCATTGTGCTCAACCCACAATGAAAAATTCATAGATTGGACGGTCTGA 275
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(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the BAC library DSM1
For BAC library availability, please contact Masa-Toshi Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Phytophthora infestans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:724q"
/clone="DSN1-015001.F.fa"
/clone_lib="DSN1 Drosophila BAC library"
                                                                                                                                                                                                                                                                                                                                                                        Saga Ippongi-cho, Ukyo-ku, Kyoto 616-8354, Japan
Tel: 81-75-873-2660 FAX: 81-75-861-0881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38.2; DB 10;
Pred. No. 1.1;
0; Mismatches 33;
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/organism="Drosophila simulans"
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University of California
Webber Hall, Riverside, CA 92521, 1
Tel: 909 787 4199
Fax: 909 787 4294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           te 2 : Sacl.
Location/Qualifiers
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1 Similarity 63.7%;
58; Conservative
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R.Site 1
R.Site 2
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Matches 58; Conservat
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PUHFI42TD ZM 0.6_1.0_KB Zea mays genomic clone ZMMBTa439G12, genomic survey sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (baess 1 to 882)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Besnick, A., Praser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 GCCTAAAGCGCAGACGCGCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCCAC 242
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                                      242
/db_xref="taxon:4577"
/clone="zmwBTa439G12"
/clone=lib="zm_06_1.0 KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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/strain="B73"
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/organism="Zea mays"
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Class: sheared ends.
Location/Qualifiers
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Unpublished (2003)
Other GSSs: PUHFL42TB
Contact: Cathy Whitelaw
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GSS.
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Zea mays
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ZMMBBb0243J34.£ ZMMBBb Zea mays genomic clone ZMMBBb0243J24 5',
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1 (bases 1 to 802)
Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
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                                                              183 GCCTAAAGCGCAGACGCCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCCAC 242
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/lolome llb="ZMMBBD"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. ssp. mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and wing, K.
Sequencing of the maize genome
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
B5721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
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Pred. No. 3.2;
0; Mismatches 92;
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Seg primer: T7
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence.
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CG401905.1 GI:34400789
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Best Local Similarity 50.0
Matches 92; Conservative
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                          581
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CG401905
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Lycopersicon esculentum (Solanum lycopersicum)

Lycopersicon esculentum

ENkaryord, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Enkaryord; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

St. (bases 1 to 991)

Mueller, L.A., Buels, R.M., Wang, Y., Tanksley, S.D., Giovannoni, J.J.,

Van Eck, J. and Stack, S.

BAC end sequencing from three Solanum lycopersicon libraries

Unpublished (2005)

Contact: Lukas Mueller

Tanksley Lab, Dept. of Plant Breeding

Cornell University

Tel: 607-255-6557

Fax: 607-255-6658

Email: sgn-feedback@sgn.cornell.edu

Plate: 1 row: I column: 13
    Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries:
humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 258B20. 258B20
is part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene. Further details:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS 11-AUG-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304628 Tomato EcoRI BAC Library Lycopersicon esculentum genomic clone SL EcoRI0001113 3, genomic survey sequence.
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Best Local Similarity 52.7%; Pred. No. 4.3;
Matches 79; Conservative 0; Mismatches 71;
                                                                                                                                                                  http://www.ganger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
                                                                                                                                                                                                              1. .768
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High quality sequence stop: 694.
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                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 956)
Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C., Schovetz, Y., Ruks, G., Yu, Y., Wing, R. and Messing, J.
Sequencing of the maize genome at PGIR (2003c)
                                                                                                                                                                                                                                                                                                                                                                           Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 TGTGGTGGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATTATGTGGCTTATTTGTT 182
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 768)
Humphray, S.J., Huckle, E. and Durham, J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="reaxon:4577"
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Danio rerio genomic clone DKEY-258E20, genomic survey sequence.
BX214284
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ZMMBBD0492E18f ZMMBBb (HindIII) Zea mays genomic clone
ZMMBBD0492E18 5', genomic survey sequence.
CGB82662 GI:38613671
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                                                                                                                                                                                                                                                                                                                                                                                                                                               190 Frelinghuygen Road, Piscataway, NJ 08854, USA
Trt: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
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/cultivar="B73"
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                                                                                                                                                                                                                                                                                                                                                   Contact: Bharti, A.K.
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Class: BAC ends
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/clone_lib="Tomato EcoRI BAC Library"
/note="Vector: unk; Site_l: EcoRI"
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1; 0; Gaps 0; 3CAGACGCC 201 3TTCAAGGG 347 AATTCATAG 261            AAAAATATAA 287	
11.9%; Score 36.4; DB 10; Length 99; S5.6%; Pred. No. 4.5; St. Indels ative 0; Mismatches 56; Indels arrangementangegerrarracemanded archaeogerrarangementangement of the property of the prop	TGTA 281
tch al Similarity 70; Conserve 142   CITATEGETTY 406   GTTTTTGTAGG 202 CAGACCCCCC 346 TGAAAACTCC 262 ATTGGA 267	286 TTTGTA 281
ury Match Str. Local Str. Ches 70 (ches 70 406 (ches 73 406 (ches 7406 (ches	286
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Search completed: January 20, 2006, 21:07:43 Job time : 3759 secs

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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
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AAB61874 ADD45030 ADD45030 ABO63032 ABM83572 ABM83572 ABM83572 ADG6323 ADC6329	AL I GNMENTS	AA.				recto regu							Henderson		cing contro	зh.	adenovirus ling sequenc ntroduced i ion of such y enhances The inventi hich prefer
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1199 1721 1728 1739 1939 1939 1939 1939 1939 1939 1939		; protein;		evised) irst entry)	protein	h protein; ADP; v in transcription carcinoma; hepato				98WO-US004084	97US-0039 98US-0003	INC.	Lamparski HG	42.	vector, f transcrip regulatory	, 102pp;	acid o . The A der, ca egion. signif produc rus vec
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		standard;		55	deat	death roteil lar c	28					Õ	Ľar	176	<b>a a</b>	Page	
255 266 276 287 288 399 391 391 391 391 391 391 391		61197	AAW61197;	27-AUG-2003 07-DEC-1998	Adenovirus d	Adenovirus death   alpha-fetoprotein   hepatocellular ca	Mastadenoviru	WO9839465-A2	11-SEP-1998.	03-MAR-1998;	03-MAR-1997; 02-MAR-1998;	(CALY-) CALYDON	Little AS,	WPI; 1998-4958 N-PSDB; AAV476	New adenovirus gene under the transcription	Claim 29; Pa	This is the adenovirus twithout the in the B3 or adenoviral viiling and competent adexpress alph
		RESULT 1 AAW61197 ID AAW XX	<b>123</b>	<b>4</b> 88	<b>3</b> 8	X K K K K	<b>18</b> 3	Y W X	<b>€</b> 2 \$	4 F	<b>EE</b>	<b>18</b> 3	{ L }	<b>3</b> 88	X	SS :	¥88888888

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the amino acid sequence of adenovirus death protein (ADP). Claimed replication-competent adenovirus (Ad) vectors comprise an Ad gene under transcriptional control of a CEA-TRE. The vectors can be used to detect and monitor samples for the presence of cells that allow a CEA-TRE to function, and to selectively kill such cells, especially malignant cells. Osciors containing an ADP gene (see AAV52966) may be more potent than vectors lacking the gene, making possible more effective treatment and/or lower dosage requirement
comprise at least one adenovirus gene, preferably a gene that contributes to cytotoxicity, under the transcriptional control of an AFP transcription regulatory element (see AAV47654-55). The vectors are useful for conferring selective cytotoxicity to AFP-expressing cells, especially cancer cells. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New adenovirus vectors, particularly for cancer therapy - comprising adenovirus gene under transcriptional control of carcinoembryonic antigen
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                                                                                                                                                                                                                                                                                                                                                           Carcinoembryonic antigen; transcriptional regulatory element; CEA-TRE; human; promoter; enhancer; vector; cancer; gene therapy; PCR; primer; adenovirus death protein; ADP.
                                                                                                                                                     MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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100.0%; Pred. No. 2.5e-61;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 68; 95pp; English
                                                                                                                                                                                                                                                                    AAW78902 standard; protein; 101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcriptional regulatory element
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                                                                                                                  Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                       Adenovirus death protein.
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                                                                                                       Local Similarity
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                                                                      Seguence 101 AA;
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This is the amino acid sequence of adenovirus death protein (ADP). Claimed replication-competent adenovirus (Ad) vectors comprise an Ad gene under transcriptional control of a probasin transcriptional response element (PB-TRE, see AAV57334). The vector can be used for detecting cells that allow a PB-TRE to function, especially cells expressing an androgen receptor, such as prostate cells. They can be used to confer selective toxicity to such cells. In particular, the vectors con be used for treating cancers such as prostate cells. They can be used to confer ADP gene (see AAV57354) may render the vector more potent, making possible more effective treatment and/or a lower dosage requirement. An Ad vector has been constructed that contains the ADP gene under control of PB-TRE. Cytotoxicity was demonstrated toward LNCaP (prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                  1 MTGSTIAPITDYRNTTATGLISALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New adenovirus vectors, particularly for cancer therapy - comprising an adenovirus gene under transcriptional control of a probasin transcriptional regulatory element.
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   MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probasin transcriptional response element; PB-TRE; rat; androgen receptor; adenovirus; vector; prostate cancer; gene therapy; adenovirus death protein; ADP.
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                                                                                                                   61 CLKRRRARPPIYRPIIVLNPHNBKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                      100.0%; Score 551; DB 2;
100.0%; Pred. No. 2.5e-61;
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                                                                                                                                                                                                                                                                                                                                     AAW75787 standard; protein; 101 AA
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Matches 101; Conservative
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The present sequence represents an adenoviral death protein, which is used to construct the vectors of the invention. The specification describes adenoviral vectors which comprise an adenovirus gene under transcriptional control of a cell status specific transcriptional regulatory element (TRE). The TRE is preferably one that is essential for adenovirus wectors may be used for the treatment of a range of tumours such as lung, stomach, breast, colon and rectum, and uterine and cervix cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adenovirus vectors comprising cell-status specific response elements useful in gene therapy protocols for the treatment of cancers.
                                                                                                        adenoviral vector; adenovirus gene; transcriptional control;
transcriptional regulatory element; TRB; adenoviral propagation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 551; DB 3; Length 101; Best Local Similarity 100.0%; Pred. No. 2.5e-61; Matches 101; Conservative 0; Mismatches 0; Indels 0
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                                                                  Amino acid sequence of an adenoviral death protein.
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                                                                                                                                                death protein; tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This protein comprises the adenovirus death protein (ADP) of adenovirus serotype 2. The invention provides novel adenovirus vectors in which at least one adenovirus gene, preferably one that contributes to cytocoxicity, is placed under transcriptional control of a human glandular kallikrein hKLK2 enhancer transcriptional regulatory element (hKLK2-TRE, see AAX24755). Such vectors are useful for treatment of cancers auch as prostate cancer. The ADP gene may render the adenoviral vector more potent, making possible more effective treatment and/or lower dosage requirement. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                              Enhancer; glandular kallikrein-1; hGK-1; hKLK2; human; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIGSTIAPITIDYRNTTATGLISALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          providing increased expression of heterologous sequences in prostatic cells, and related adenoviral vectors for treating prostatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid containing the human glandular kallikrein enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 551; DB 2; Length 101; 100.0%; Pred. No. 2.5e-61; ive 0; Mismatches 0; Indels
CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 165-166; 179pp; English.
                                                                                                                         AAW98003 standard; protein; 101 AA
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                                                                                                                                                                                                                                                                                                                               therapy; adenovirus death protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schuur ER
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98US-0076545P.
98US-00127834.
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                                                                                                                                                                                                                             (first entry)
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Matches 101; Conservative
                                                                                                                                                                                                                                                                        Adenovirus death protein.
                                                                                                                                                                                                                                                                                                                                                                          Human adenovirus type 2.
                                                                                                                                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yu D, Herdenson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-153804/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 101 AA;
                                                                                                                                                                                                        17-OCT-2003
21-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                  WO9906576-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1998;
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AAY84407;

RESULT 5
AAY84407
ID AAY8
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AC AAY8

Query Match

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Gaps

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Adenovirus death protein; uroplakin II; vector; transcriptional regulatory element; TRE; urothelial cell; bladder cancer;

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Human adenovirus type

WO200172994-A2

04-OCT-2001

human; gene therapy.

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The invention relates to a recombinant vector (VI) which is replication-
competent in a neoplastic cell and which overexpresses an adenovirus
death protein (ADP). The vector can be used in a method for promoting
death of a neoplastic cell that comprises contacting the neoplastic cell
vith at least one VI; and a composition comprising VI and a second
recombination virus which is: (a) replication defective and which
expresses an anti-cancer gene product, where VI complements replication
of the second recombinant virus; or (b) replication-competent in a
neoplastic cell. VI, together with one or more replication-defective
adenovirus which expresses an anti-cancer gene product, are useful in
cancer therapy. Overexpression of ADP by VI results in faster lysis of
cells and spread of the virus throughout a cell monolayer than viruses
expressing wild-type levels of ADP. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant vector which is replication-competent in a neoplastic cell and overexpresses an adenovirus death protein, useful in cancer therapy when used together with replication-defective adenovirus which expresses
                                                                      /note= "transmembrane domain (AAB61874); fragment specifically claimed for"
                                                                                                                                              63. 70
/note= "cytosolic basic proline domain (AAB61875)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 101;
'note= "putative lumenal domain (AAB61873)"
                                    "fragment specifically claimed for"
                                                                                                                           /note= "cytoplasmic-nucleoplasmic domain"
                                                                                                                                                                                    fragment specifically claimed for"
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100.0%; Pred. No. 2.5e-61;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                     Tollefson AE
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                                                                                                                                                                                                                                                                                                                                                                                                       Toth K, Doronin K,
                                                                                                                                                                                                                                                                                            12-JUL-2000; 2000WO-US018971.
                                                     .59
                                                                                                                                                                                                                                                                                                                                                                  (UYSL-) UNIV SAINT LOUIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an anti-cancer gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-103079/11.
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Best Local Similarity
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                                                                                                                                                                                                                      WO200104282-A2
                                                                                                                                                                                                                                                          18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                       Wold WSM,
                  Peptide
                                                                                                              Domain
                                                       Domain
                                                                                                                                                Domain
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Human urothelial cell specific uroplakin transcriptional regulatory sequences, useful for producing adenoviral vectors which can be used to confer selective cytotoxicity to target cells, especially bladder cancer

Henderson DR;

Zhang H,

Υu D,

(CALY-) CALYDON INC

WPI; 2001-639229/73.

N-PSDB; AAI70186.

21-MAR-2001; 2001WO-US009224. 24-MAR-2000; 2000US-0191861P Example 6; Fig 12; 147pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of the adenovirus death protein (ADP). The ADP gene coding region (see AAI70186) was obtained by PCR amplification and used in the construction of adenoviral vectors in which ADP expression was under the control of a urothelial cell-specific transcriptional regulatory element (TRE) derived from the human uroplakin II gene 5' flanking region (see AAI70144). This is an example of preferably an adenovirus gene, under transcriptional control of a urothelial cell-specific TRE. They display urothelial cell-specific cytotoxicity, and are used for the specific, targeted gene therapy of bladder cancer. (Updated on 11-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adenovirus, ADP; replication-competent, adenoviral vector, TRE, transcriptional regulatory element; mutation; deletion, IRES; promoter; internal ribosome entry site; cytotoxic; cancer; bladder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unidentified adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 101 AA;
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Gaps

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101; Conservative

1 MIGSTIAPITDYRNTIATGLISALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC

CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101 CLKRRRARPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

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AAM50206 standard; protein; 101 AA

(first entry)

(revised)

11-SEP-2003 07-JAN-2002

AAM50206;

AAM50206
ID AAM5
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AC AAM5
XX
DT 11-6
DT 07-4
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Adenovirus death protein

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US2003044383-A1
  Unidentified.
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                                                                                                                                                                                                                                                                                 This sequence represents adenoviral ADP. The ADP coding sequence may be used in the replication-competent adenoviral vector (A) of the invention which contains two genes (G1, G2) that are co-transcribed as a single mRNA and under control of a heterologous, target cell-specific transcriptional regulatory element (TRE). G2 has a mutation in, or deletion of, its endogenous promoter and is controlled from an internal ribosome entry site (IRES). The ADP coding sequence may be used as G1 or G2. (A) has greater specificity for a target cell than a similar vector in which TRE is operably linked to a gene and which lacks an IRES. (A) are used to modify the genotype of target cells, optionally in vitro with subsequent return of altered cells to the host and where G2 is a cytotoxic gene, to confer selective cytotoxicity to target cells, especially for killing cancer cells. On the displays a cytotoxic, cespecially for killing cancer cells. Abp displays a cytotoxic, or specific TRE ansures that (A) has better targeting specificity, with minimal replication in non-target cells, so a runaway infection is prevented but production of adenoviral proteins in target cells activates cand/or stimulates the immune response against target cells producing such proteins. The use of an IRES (rather than two identical control elements) eliminates the risk of homologous recombination and may provide enough a certification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIGSTIAPTIDYRNTTATGLISAINLPQVHAFVNDWASLDMWWFSIAIMFVCLIIMWLIC 60
                                                                                                                                                                                                      Replication-competent adenoviral vector, useful e.g. for killing cancer cells, contains two genes linked by internal ribosome entry site and controlled by target-specific regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTGSTIAPTTDYRNTTATGLTSALNEPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adenovirus; transcriptional regulatory element; TRE; prostate; liver; breast cancer; colon cancer; antitumour; adenovirus death protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 551; DB 4; Length 101; 100.0%; Pred. No. 2.5e-61; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG69353 standard; protein; 101 AA
                                                                                                                                                                                                                                                            Disclosure, Fig 9; 148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adenovirus death protein (ADP).
                                                     21-MAR-2001; 2001WO-US009036.
                                                                               24-MAR-2000; 2000US-0192156P
                                                                                                                                     Li Y, Henderson DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity 100.7
Matches 101, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to standardise OS field)
                                                                                                                                                              WPI; 2001-639234/73.
                                                                                                          (CALY-) CALYDON INC
                                                                                                                                                                              N-PSDB; AAH43535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 101 AA;
WO200173093-A2
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                          04-OCT-2001
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The invention relates to an adenovirus vector (AV) comprising an AV gene under transcriptional control of a cell type-specific transcriptional regulatory element (TRE) and optionally a first AV gene under control of a first cell type-specific TRE and a second gene under control of second cell type-specific TRE where the first and second cell type-specific TREs are substantially identical. When the vector is introduced into a cell (e.g. prostate cell, liver cell, breast cancer cell or colon cancer cell) it allows the cell type-specific TRE to function, resulting in cytotoxicity. The vector is useful for suppressing tumour growth of a target cell. This sequence represents a polypeptide used in the scope of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel adenovirus vector comprises adenovirus gene under transcriptional control of cell-type specific transcriptional response element for conferring selective toxicity on target cell and for suppressing tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adenoviral vector; adenovirus gene; transcriptional control; TRE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 551; DB 5; Length 101; 100.0%; Pred. No. 2.5e-61; ive 0; Mismatches 0; Indels
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                                                                                                                                        06-DEC-2000; 2000US-00732169.
                                                                                                                                                                                                              98US-00151376.
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Best Local Similarity 100.
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                (HEND/) HENDERSON D (SCHU/) SCHUUR E R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-582468/62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABK99587
US2002068049-A1
                                                                                                                                                                                                                                                                                                                                                                                       Henderson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the invention
                                                                                                                                                                                                              10-SEP-1998;
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                                                                     36-JUN-2002
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                              adenovirus gene under transcriptional control of a cell type-specific transcriptional response element (TRE). Example TRES given in the specification include human prostate-specific antigen (ESA) TRE, human glandular kallikrein (hKLK) TRE, rat probastin (PB) TRE, human carcinoembryonic antigen (CEA) TRE, and human mucin-like glycoprotein DF3 (MUC1) TRE. The modified adenovirus vector is useful as a vehicle for introducing new genetic capability, particularly associated with cytotoxicity for treating neoplasia. For example, the vector may be used in a target cell to suppress tumour growth, or to kill the target cell. The vector is particularly useful in gene therapy. The present sequence represents adenovirus death protein (ADP). (Updated on 23-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MIGSTIAPITDYRNTTATGLISALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
                                                                                                                                                                                                                                                                                New adenovirus vector for transfecting target host cells, comprises ar
adenovirus gene under transcriptional control of a cell type-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; prostate; transcriptional response element; TRE; polyethylene glycol; PEG; masking agent; tumour cell growth; proliferation; psoriatic lesion; wound healing; hyperplasia; cancer; cytostatic; antipsoriatic; vulnerary; ADP.
                                                                                                                                                                                                                                                                                                                                                       The present invention relates to adenoviral vectors comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 551; DB 6; Length 101; 100.0%; Pred. No. 2.5e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ADP protein sequence SeqID 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADI36347 standard; protein; 101 AA.
                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 19; 83pp; English
                                                                                                                                                                                                                                                                                                        transcriptional response element
                                                                                97US-0039597P.
97US-0039599P.
97US-0039762P.
97US-0039763P.
                                                                                                                                 98US-00033333
98US-00033428
                                   98US-00151376
                                                         95US-00495034
96US-00699753
                                                                                                                                                           98US-00033555
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                                                                                                                                                                                                                     Henderson DR, Schuur ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 101; Conservative
                                                                                                                                                                                   HENDERSON D R.
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Best Local Similarity
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                                                                                                                                                                                                                                           WPI; 2003-456547/43.
N-PSDB; ACD07312.
                                                                                                                                                                                             SCHUUR E R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 101 AA;
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                                                                                03-MAR-1997;
03-MAR-1997;
03-MAR-1997;
03-MAR-1997;
                                  10-SEP-1998;
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           06-MAR-2003.
                                                                                                                                 02-MAR-1998
02-MAR-1998
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                                                                                                                                                                                             (SCHIU/)
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AD136347
1D AD136
XX
AC AD136
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DT 22-AP
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HUMAN
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KW HUMAN
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This invention relates to a novel composition that contains a replication competent adenovirus capable of transfecting target host cells.

Specifically, it comprises an adenoviral gene essential for replication (ELA, ELB or EA), which is under the transcriptional control of a prostate specific transcriptional response element (TRE) and polyethylene composition as the masking agent. The present invention describes this composition as useful for suppressing tumour cell growth and for lowering the levels of tumour cell markers. It can also be used for introducing transiant expression that may be involved in treating undesirred proliferations other than tumours, such as psoriatic lesions and wound healing. In addition, it is useful for detecting cells where a cell type-specific TRE is functional in a biological sample and for treating prostate-associated diseases such as hyperplasia and cancer. As such, these compositions exhibit cytostatic, antipsoriatic and vulnerary activities. This polypeptide sequence is the human ADP protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition comprising replication competent adenovirus having adenovirus gene essential for replication under transcriptional control of cell type specific transcriptional response element and masking agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 551; DB 8; Length 101; Best Local Similarity 100.0%; Pred. No. 2.5e-61; Matches 101; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Little AS, Lamparski HG, Henderson DR, Schuur ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 11; 115pp; English
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                                                                                                                                  27-JUN-1995; 95US-00495034.
26-JUN-1996; 96US-00669753.
03-MAR-1997; 97US-0039597P.
03-MAR-1997; 97US-0039762P.
02-MAR-1998; 98US-00033333.
02-MAR-1998; 98US-00033555.
10-SEP-1998; 98US-00033555.
10-SEP-1998; 98US-00033555.
                                                                 02-MAY-2002; 2002US-00139089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LITTLE A S.
LAMPARSKI H G.
HENDERSON D R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-119002/12.
N-PSDB; ADI36417.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 101 AA;
14-AUG-2003
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(LAMP/)
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Gene therapy; vector; prostate tumor; cytostatic; vasotropic; vulnerary;

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The present invention relates to an adenovirus vector comprising an adenovirus early gene essential for propagation under the control of a human prostate specific antigen promoter and a human prostate specific antigen (PSA) enhancer. The invention is useful for treating a patient suffering from prostate cancer and for making mammalian hosts that are transfently transgenic and for detecting the presence of cells that permit the function of a cell type-specific transcriptional regulatory element (TRR) in a sample. The invention is also used in the gene therapy and also as vaccine. The present sequence is the adenovirus death protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                           Vector; gene transfer; cloning vehicle; genetic engineering; prostate cancer; gene therapy; vaccine; cytostatic; prostate-specific antigen; TES; transcriptional regulatory element; PSE; prostate specific enhancer; PSA; prostate specific antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New adenovirus vector comprising an adenovirus early gene essential for propagation under the control of a human prostate specific antigen promoter and a human prostate specific antigen enhancer, for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MIGSTIAPTIDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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                               Adenovirus death protein (ADP).
                                                                                                                          adenovirus death protein; ADP
                                                                                                                                                                                                                                                     13-APR-2004; 2004US-00822873.
                                                                                                                                                                                                                                                                                                  26-JUN-1996; 96US-00669753.
10-SEP-1998; 98US-00151376.
06-DEC-2000; 2000US-00732169.
                                                                                                                                                                                                                                                                                       95US-00495034
(first entry)
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                                                                                                                                                          unidentified adenovirus.
                                                                                                                                                                                                                                                                                                                                                                   (HEND/) HENDERSON D R.
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                                                                                                                                                                                                                                                                                                                                                                                       SCHUUR E R.
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                                                                                                                                                                                        US2004241857-A1
                                                                                                                                                                                                                                                                                     27-JUN-1995;
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Adenovirus death protein.

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The present sequence in the process and inducible transcriptional transactivator (TT) coding sequence under the inducible transcriptional transactivator (TT) coding sequence under the inducible transcriptional control of a cell type-specific TRE (CT-TRE); and an adamovirus gene is preferably a gene essential for ademoviral captor. The ademovirus gene is preferably a gene essential for ademoviral replication. The TT may be inhibited or activated by the inducing agent. Also claimed is an ademovirus vector comprising: an inducible TT coding sequence under transcriptional control of a second TRE, where the TT and a second gene under transcriptional control of a second gene may an ademovirus second gene under transcriptional control of a second gene may an ademovirus control of a second gene may an ademovirus gene is activated by an exogenous inducing agent. The second gene may an ademovirus gene is under transcriptional control of a second gene whole the regulated TRE and a polymorleotide encoding an ADP cuttransactivated regulated TRE and a polymorleotide encoding an ADP under control of a second transactivator regulated TRE, where the ademovirus gene is essential for replication. Also claimed are host cells comprising the replication competent ademovirus vector, and methods for propagating and regulating the vector. A claimed method and administering are inducing agent such that the ademovirus vector is propagated and competent ademovirus vector is propagated and caused lumnne response, resistance to infection, production of a crepair, enhanced immune response, resistance to infection, production of factors, enhanced immune response, resistance of infection, production of the viral for replication of metabolic or other physiological pathways, or comparison of activity of cells in the envention of a viral gene envential for replication of a viral centerial pathways or comparison of activity of cells in the envention of a viral centerial pathways or comparison of a viral centerial pathways or comparison of a viral 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New replication competent adenovirus vector comprising an inducible transcriptional transactivator coding sequence and an adenovirus gene, useful for treating cancer, psoriatic lesions, restenosis or wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the protein sequence of adenovirus death
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                         antipsoriatic; antimicrobial; immunomodulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 11; 66pp; English.
                                                                                                                                                                                                                   24-FEB-2004; 2004WO-US005518.
                                                                                                                                                                                                                                                              24-FEB-2003; 2003US-0450232P
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Matches 101; Conservative
                                                                                                                                                                                                                                                                                                              (CELL-) CELL GENESYS INC.
                                                                      ď
                                                                      Human adenovirus type
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셤
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Novel isolated polynucleotide comprising nucleotide sequence of yeast cytosine deaminase/mutant SR 39 herpes simplex virus type 1 thymidine kinase fusion gene, useful for treating mammalian patient having malignancy or solid tumor.
                                                chemotherapy; cytosine deaminase; thymidine kinase; death protein;
                         Amino acid sequence of adenovirus type 5 adenovirus death protein.
                                                               cancer; neoplasm; 5-fluorocytosine; ganciclovir.
                                                                                                                                          /note= "Ala encoded by AAG"
                                                                                                   ,
Misc-difference 63
                                                                                                                                                                                                                                                                       (FORD-) FORD HEALTH SYSTEM HENRY
                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Page 54; 62pp; English.
                                                                                                                                                                                                                                              09-JUL-2003; 2003US-0486219P.
                                                                                                                                                                                                                      09-JUL-2004; 2004WO-US022320
07-APR-2005 (first entry)
                                                                                       Human adenovirus type
                                                                                                                                                                                                                                                                                                 Kim JH,
                                                                                                                                                                                                                                                                                                                           WPI; 2005-101983/11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 101 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the amino acid sequence of adenovirus death protein (ADP). The invention provides replication-competent adenovirus vectors specific for target cells and methods of using such vectors. The vectors contain heterologous transcription regulatory elements (TREs) and may incorporate a gene, such as the ADP gene (see AAV53632), which can contribute to cytocoxicity in the target cell. Adenoviral replication can be restricted to target cells in which the heterologous TREs are functional and thus the vectors can provide selective cytotoxicity to the target cells (e.g. prostate, liver, breast or colon), particularly neoplastic cells
                                                                                                                                                                    Adenovirus death protein; ADP; transcription regulatory element; vector; breast cancer; prostate cancer; liver cancer; colon cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New adenovirus vectors, used for treating tumours - comprising first and second adenovirus genes under control of different heterologous
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CLKRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLOYD 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcriptional regulatory elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 94; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       Lamparski HG
                                                                AAW59925 standard; protein; 101
                                                                                                                                                                                                                                                                                                             97US-0039762P.
97US-0039763P.
97US-0054523P.
98US-00033556.
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                                                                                                                  (first entry)
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Matches 100; Conservative
                                                                                                                                            Adenovirus death protein.
                                                                                                                                                                                                                                                                                                                                                                                                      Henderson DR, Yu D,
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                                                                                                                                                                                                                                                                                                                                                                              (CALY-) CALYDON INC
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Barton K, Paielli D;

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The specification describes a polynucleotide comprising a nucleotide sequence of yeast cytosine deaminase/mutant SR39 herpes simplex virus type 1 thymidine kinase fusion gene, and further comprising an adenovirus type 1 thymidine by protein gene. The polynucleotide of the invention limits the side effects of cancer treatment by using only lower doses of radiation. The polypeptide encoded by the above polynucleotide is useful for converting 5-fluorocytosine or ganciclovir into active chemotherapeutic agents. Pharmaceutical compositions comprising recombinant adenoviruses comprising polynucleotides of the invention are tumor. The present sequence represents an adenovirus type 5 adenovirus death protein, which is used to construct polynucleotides of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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ADW28321 standard; protein; 101

RESULT 15 ADW28321

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## November 2005

generate two sets of results each. The Published_Applications databases have been split into two parts to Published Applications Nucleic Acid and Published Applications Amino Acid database searches now reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published Applications Main databases. Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New). This Page Blank (uspto)

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Copyright (c) 1993 - 2006 Compugen Ltd.
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US-11-127-832-5

US-11-066-480-5

US-11-066-480-5

US-10-0857-780-4

US-11-0750-623-49060

US-10-750-185-47255

US-10-750-185-47255

US-10-750-185-47255

US-11-136-527-4007

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1717373 182031 182323 1551323 165883 1065883 1065883 1065883 10658 11658 1175 1175 1175 1175 1175 1175 1175 11	SULT 1  -11-127-832-3 Sequence 3, Application US/1112 Sequence 3, Application US/1112 APPLICANT: Hearing, Patrick APPLICANT: Hearing, Patrick APPLICANT: Banhou, Wadie APPLICANT: Gandalon, Ziv APPLICANT: Gandalon, Ziv APPLICANT: Gratenko, Dmitri TITLE REFERENCE: STONYB-04970 CURRENT APPLICATION NUMBER: US/OF PRIOR APPLICATION NUMBER: US/OF PRIOR FILING DATE: 2001-02-12 PRIOR APPLICATION NUMBER: US/OF PRIOR FILING DATE: 2001-02-12 PRIOR APPLICATION NUMBER: US/OF PRIOR FILING DATE: 2001-02-12 SOFTWARE: PATENTING DATE: 2001-02-12 SOFTWARE: PATENTING DATE: 2001-03-12 SOFTWARE: PATENTIN VERSION 3.0	100.0%; Score 307; DB 8; Length 35937; imilarity 100.0%; Pred. No. 1.96-96; Indels 0; Gaps conservative 0; Mismatches 0; Indels 0; Gaps GATGACCGGCTCAACGGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT [	CATGLOGIGGITTTCCATAGCGCTTATTTGTTTTGCCTTATTATTATGTGGGCTTATTTG
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	SULT 1 -11-127-832-3 Sequence 3, Application US Sequence 3, Application US Sequence 3, Application US SEQUENCE 1	Similarity Similarity 7; Conser GATGACGG GATGACGGG AACATCTGC	3=
000000000000000000000000000000000000000	12-3 No. App. No. App	2-3 b Sim 07; 7 GA 1 AA 1 AA	
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Sequence 4, Application US/11127832
; Sequence 4, Application US/11127832
; Publication No. US20060008884A1
; GENERAL INFORMATION:
    APPLICANT: Hearing, Patrick
; APPLICANT: Bahou, Wadie
    APPLICANT: Sandalon, Ziv
; APPLICANT: Sandalon, Ziv
; APPLICANT: Gantenko, Dmitri
; TITLE OF INVENTION: Adenoviral Vectors
; TITLE OF INVENTION: Adenoviral
; TITLE OF INVENTION: ADMINER: US/11/127,832
; CURRENT APPLICATION NUMBER: US/09/782,378
; PRIOR FILING DATE: 2001-02-12
; RUGHRAND: APPLICATION NUMBER: 60/237,747
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SEQ ID NO 4
LENGTH: 35935
                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-860-436-2
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ACACAATGAAAAATTCATAGATTGGACGGTCTGAAAACCATGTTCTCTTTTTACAGTA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhou, Jianfeng
APPLICANT: Zhou, Jianfeng
APPLICANT: Lu, Yunping
APPLICANT: Lu, Yunping
APPLICANT: Chen Gang
APPLICANT: Gao, Ginglei
APPLICANT: Gao, Ginglei
TITLE OF INVENTION: ONSTRUCT OF TUMOR-SELECTIVE RECOMBINANT
TITLE OF INVENTION: ADENOVIRUS, METHODS FOR PREPARING THE SAME
TITLE OF INVENTION: ADENOVIRUS, METHODS FOR PREPARING THE SAME
TITLE OF INVENTION: ADENOVIRUS, METHODS FOR PREPARING THE SAME
TITLE OF INVENTION: ADENOVIRUS, METHODS FOR PREPARING THE SAME
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Pred. No. 1.2e-57;
0; Mismatches 35; Indels 1
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Sequence 2, Application US/10860436

Publication No. US2050271622A1

GENERAL INFORMATION:
APPLICANT: Zhou, Jianfeng
APPLICANT: Ma, Ding
APPLICANT: Wang, Shixuan
APPLICANT: Wang, Shixuan
APPLICANT: Chen, Gang
APPLICANT: Gao, Ginglei
APPLICANT: Gao, Ginglei
TITLE OF INVENTION: CONSTRUCT OF TUMOR-SELECTIVE RECOMBINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29514 retrireterracagiatearraa 29537
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ORGANISM: Artificial Sequence
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Best Local Similarity 86.4%;
Matches 228; Conservative
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LENGTH: 35696
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TITLE OF INVENTION: ADENOVIRUS, METHODS FOR PREPARING THE SAME TITLE OF INVENTION: AND USES THEREOF PELB REFERENCE: 850141.402 CURRENT APPLICATION NUMBER: US/10/860,436 CURRENT FILLING DATE: 2004-06-03 NUMBER OF SEQ ID NOS: 15 SOFTWARE PASISEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 35893
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.8%; Score 196; DB 7;
Best Local Similarity 86.4%; Pred. No. 1.2e-57;
Matches 228; Conservative 0; Mismatches 35
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 TCATTGTGCTCAACCCACACAATGAAAAATTCATAGATTGGACGGTCTGAAAC-CATGT
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                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hearing, Patrick
APPLICANT: Bahou, Wadie
APPLICANT: Bahou, Wadie
APPLICANT: Bandalon, Ziv
APPLICANT: Sandalon, Ziv
TITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STOWNE-04970
CURRENT APPLICATION NUMBER: US/01/127,832
CURRENT FILING DATE: 2005-05-12
PRIOR PILING DATE: 2001-02-12
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Version 3.0
SEQ ID NO 5
                                                                                                                                                                                                                               29753 TCTTTTCTCTTACAGTATGATTAA 29776
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                                                                                                                                                                                                                                                                                                                               ; Sequence 5, Application US/11127832; Publication No. US20060008884A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application US/11066480; Publication No. US20050282280A1; GENERAL INFORMATION: APPLICANT: ENNIST, DAVID LEONARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Human adenovirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 35935
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US-11-066-480-5
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OTHER INFORMATION: 28781 to 29952 of Ar20-1007 including the E3-6.7 gene, and the hu OTHER INFORMATION: man GM-CSF cDNA
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APPLICANT: RAMBERS, STEFAN M.
APPLICANT: RAMBERS, STEFAN M.
APPLICANT: RAMBERS, STEFAN M.
APPLICANT: RENELAND, RIKARD HERRY
APPLICANT: RENELAND, RIKARD HERRY
APPLICANT: RENELAND, RIKARD HERRY
APPLICANT: HOYAL-WRIGHTSON, CAROLIN R.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION UNMERR: US/10/857,780
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT FILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-01-24
PRIOR FILING DATE: 2003-01-24
PRIOR FILING DATE: 2003-01-25
PRIOR FILING DATE: 2003-01-25
PRIOR FILING DATE: 2003-11-25
SOFTWARE: PATENTIN VOYESION 3.2
SEQ ID NO 4
LENGTH 191350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   988 CCGCCCTACCCGACTTACATCTACCACAATACACCCCCAAGTTTCTGCCTTTGTCAATA 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1048 ACTGGGATAACTTGGGCATGTGGTGGTTCTCCATAGCGCTTATGTTTTTATGTATTA 1107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 TTATGTGGCTTATTTGTTGCCTAAAGCGCAGACGCGCCAGACCCCCCCATCTATAGGCCTA 224
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TITLE OF INVENTION: ONCOLVTIC ADENOVIRAL ENCODING GM-CSF FILE REFERENCE: GTIN-001
CURRENT APPLICATION NUMBER: US/11/066,480
CURRENT FILING DATE: 2005-02-28
PRIOR APPLICATION NUMBER: US/10/925,205
PRIOR FILING DATE: 2004-08-23
PRIOR FILING DATE: 2004-08-28
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NOS: 22
LENGTH: 1172
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16914)..(16914)
FEATURE:
FEATURE:
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ORGANISM: artificial sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wpeth;
; APPLICANT: Woute, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086;)
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR PLING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; EBO ID NO 3556
; LENGTH: 2926
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APPLICANT: MU GENOMICS, INC.
APPLICANT: MU GENOMICS, INC.
APPLICANT: MU GENOMICS, SUE K.
APPLICANT: RERR, Richard
APPLICANT: MOSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REPRENCE: MMIL100-2-31
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT PILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN VETSION 3.1
IENGTH: 972
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.8%; Score 33.2; DB 8; Length 2926; Best Local Similarity 59.6%; Pred. No. 0.31; Matches 56; Conservative 0; Mismatches 38; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.2%; Score 31.2; DB 7; Length 872; Best Local Similarity 55.6%; Pred. No. 0.85; Matches 60; Conservative 0; Mismatches 48; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Bovine 19866881284640
                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-750-185-49060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 TGTGGCTTATTTGTTGCCTAAAGCGCAGACGCCCAGACCCCCCATCTATAGGCCTATCA 227
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! LOCATION: (117565)..(117565)
! OTHER INFORMATION: n is a, c, g, or t
US-10-857-780-4
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                          LOCATION: (19266)..(19266)
OTHER INFORMATION: n is a, c, g,
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NAME/KEY: misc_feature
LOCATION: (61207)
OTHER INFORMATION: n is a, c,
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LOCATION: (34467)..(34472)
OTHER INFORMATION: n is a, c,
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LOCATION: (103359)..(103359)
OTHER INFORMATION: n is a, c,
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LOCATION: (95893)..(95893)
OTHER INFORMATION: n is a,
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NAME/KEY: misc_feature
LOCATION: (57355)..(57355)
OTHER INFORMATION: n is a,
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LOCATION: (64980)..(64980)
OTHER INFORMATION: n is a,
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NAME/KEY: misc_feature
LOCATION: (64987) ..(64987)
OTHER INFORMATION: n is a,
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LOCATION: (81452)..(81452)
OTHER INFORMATION: n is a,
                                                                                         NAME/KEY: misc feature
LOCATION: (26334)..(26334)
OTHER INFORMATION: n is a,
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NAME/KEY: misc_feature
LOCATION: (38627) ..(38628)
OTHER INFORMATION: n is a,
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LOCATION: (40555)..(40555)
OTHER INFORMATION: n is a,
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          misc feature
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Best Local Similarity
Matches 68; Conserva
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RESULT 10 US-10-750-623-49060 ; Sequence 49060, Application US/10750623

RESULT 8 US-11-136-527-3556/c ; Sequence 3556, Application US/11136527

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264 TGGACGGTCTGAAACCATGTTCTCTTTTTACAGTATG 302
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; ORGANISM: Bovine 19866880533767
US-10-750-623-47255
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                                                                                                                                       APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
FILLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR PPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 CGCTTATGTTTGCCTTATTATTATGTGGCCTTATTTGTTGCCTAA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     651 récararcaaacearcécharitrirearchechacearchigecaaa 698
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10.2%; Score 31.2; DB 7; Length 872;
Best Local Similarity 55.6%; Pred. No. 0.85;
Matches 60; Conservative 0; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.1%; Score 31; DB 7; Length 1542; 49.7%; Pred. No. 1.3;
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Publication No. US20050260603A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Bovine 19866881284640
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; ORGANISM: Bovine 19866880533767
US-10-750-185-47255
     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENPELD, David
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 49060
LENGTH: 872
No. US20050287531A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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Matches 79; Conservative
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US-10-750-185-47255
                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 CATCCATTCTTTAAAAAATATTGTTTTGCTGAATACTTGAAAGTGAATTGCATATATCA 489
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Sequence 4007, Application US/11136527

Publication No. US2000287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

TILLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031896-041000 (AM101086)

CURRENT FILING DATE: 2005-55-25

PRIOR PILING DATE: 2005-55-25

PRIOR FILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: PARENTIN Version 3.2

LENGTH: 1009
                                                                                                                        Sequence 47255, Application US/10750623

Publication No. US20050287531A1

GENERAL INFORMATION:

APPLICANT: MI EMORINE, INC.

APPLICANT: RERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David

APPLICANT: FANTIN, Dennis

TILLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MAILIOG-1

CURRENT PILING DATE: 2003-12-31

FRIOR APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SEQ ID NO 47255

LENGTH: 1542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.1%; Score 31; DB 7; Length 1542; Best Local Similarity 49.7%; Pred. No. 1.3; Matches 79; Conservative 0; Mismatches 80; Indels
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APPLICATION NUMBER: PCT/US03/29906

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Search completed: January 20, 2006, 21:30:39
Job time : 397 secs
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; Sequence 8103, Application US/11136527
; Publication No. US2000287570A1
; GENERAL INFORMATION:
APPLICANT: Wyeth
; APPLICANT: Wounte, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SEQ ID NOS: 362830
; SEQ ID NO 8103
; TENNER: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 AAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGACATGTGGTGGTFT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 AACATCATCCCTGGCACTGACCTAAGCAAGAATCAGGCCATGAAGGAAAAGGAGAGGCT 235
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                                            176 AACATCATCCCCTGGCACTGACCTAAGCAAGAATCAGGCCATGAAGGAAAAGGAGAGGCT 235
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133 TICCATAGCGCTTATGTTTGCCTTATTATTATGTGGCTTATTTGTTGCCTAAAGCG 192
                                                                                                                                           236 GATTAAAGAGCTGCAGCTCATTACCGAGGAGAAAAATGACCTGAGAGATCGCCTGAAGTT 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 AATTCATAGATTGGACG 269
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                                                                                                                                                                                                                                                                                                                                       356 CCTGGAGAGATGGAGG 372
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Sequence 1, Application US/11091018
Sequence 1, Application US/11091018
Publication No. US20050287551A1
Sequence 1, Nepration 10220050287551A1
APPLICANT: Greatersdottir, Solveig
APPLICANT: Thorleifsson, Gudmar
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
TITLE OF INVENTION: METHODS OF TREATMENT
TITLE OF INVENTION: METHODS OF TREATMENT
CURRENT APPLICATION NUMBER: US/11/091,018
CURRENT FILING DATE: 2005-01-25

US-11-091-018-1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 TACCGGACTAACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGC 111
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Pred. No. 73;
0; Mismatches 78; Indels 0; 0
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PRIOR FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: 10/255,120
PRIOR FILING DATE: 2002-09-25
PRIOR FILING DATE: 2003-09-25
PRIOR FILING DATE: 2003-04-18
PRIOR FILING DATE: 2003-04-18
PRIOR FILING DATE: 2003-08-27
PRIOR FILING DATE: 2002-02-04
PRIOR FILING DATE: 2002-04
PRIOR PILING DATE: 2001-03-19
NUMBER: OF SEQ ID NOS: 102
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(1691140)
; OTHER INFORMATION: n=A,T,C or G
US-11-091-018-1
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Best Local Similarity 49.7%;
Matches 77; Conservative
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                             LENGTH: 1691140
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2, Appli 4, 3, Appli 5, Appli 6, Appli 11, Appli 12, Appli 12, Appli 130, Appli 25, Appli 26, Appli 26, Appli 26, Appli 27, Appli 26, Appli 26, Appli 27, Appli 28, Appli 28, Appli 29, Appli 26, Appli 26, Appli 26, Appli 26, Appli

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

US-10-860-630-2 US-09-725-720-43 US-09-782-378A-4 US-09-782-378A-5 US-10-264-839-12 US-10-432-989-11 US-10-432-981-11 US-10-432-981-11 US-10-492-178-9 US-10-492-178-9 US-10-492-178-9 US-10-492-178-9 US-10-492-178-9 US-10-95-535-1 US-10-94-514A-732 US-10-94-54-514A-732 US-10-94-496-21 US-10-94-496-30 US-10-94-496-30 US-10-982-06-30

Sequence Sequence Sequence Sequence Sequence

US-10-636-730-30 US-09-952-060-25 US-10-380-641-25

ALIGNMENTS

Sequence Sequence Sequence Sequence Sequence Sequence

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APPLICANT: Yu, De Chao
APPLICANT: Yu, De Chao
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: Adenovirus Vectors Containing Cell
TITLE OF INVENTION: Adenovirus Vectors Slements and Methods of Use Thereof
FILE REFERENCE: 348022001200
CURRENT APPLICATION NUMBER: US/09/392,822
CURRENT PILING DATE: 1999-09-09
EARLIER FILING DATE: 1998-09-10
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCCTTTGTCAATGACTGGGCGAGCTTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CATGIGGIGGITTICCATAGCGCTTAIGITIGITTIGCCTTATTATTATGTGGCTTATTIG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTTCTTTTACAGTA 300
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100.0%; Pred. No. 2.3e-91;
iive 0; Mismatches 0;
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Patent No. US20010053352A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 307; Conservative
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US-09-392-822-8
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NAME/KEY: CDS
LOCATION: (2)
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Sequence 15, Appl
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                                                                                                            ; Search time 803 Seconds (without alignments) 3161.518 Million cell updates/sec
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Sequence 5, App
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Sequence 10,
Sequence 61,
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Sequence 61,
Sequence 7, A
Sequence 2, A
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1: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USOPB_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USOPB_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-09-814-292-3

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US-09-151-376-11

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US-10-045-116-19

US-10-139-089-10

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US-10-822-873-61

US-10-822-873-61

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US-10-938-227-7

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Maximum Match 100%
Listing first 45 summaries
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Length 307; Indels 9 9 120

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TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF
                                   CURRENT PELLING DATE: 2001-06-05
CURRENT FILING DATE: 2001-06-05
PRIOR PELLING DATE: 2001-06-05
PRIOR FILING DATE: 1998-08-03
PRIOR FILING DATE: 1998-08-03
PRIOR PLING DATE: 1998-08-05
PRIOR FLING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 4
LENGTH: 307
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COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSES: MORRISON & FOER:
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
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Lamparski, Henry
Schuur, Eric
                      FILE REFERENCE: 348022000900
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LOCATION: (2)..(307)
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                                                                                                                                                                                              Sequence 3. Application US/09814292

| Sequence 3. Application US/09814292
| Patent No. US20020120117A1
| Patent No. US20020120117A1
| GENERAL INFORMATION:
| APPLICANT: Yu, De-Chao
| APPLICANT: Yu, De-Chao
| APPLICANT: Yu, De-Chao
| TITLE OF INVENTION: HUMAN UNCOPLARIN-ELAL CELL SPECIFIC UROPLAKIN
| TITLE OF INVENTION: HUMAN UNCOPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, TITLE OF INVENTION: WROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
| TITLE OF INVENTION: WROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
| TITLE OF INVENTION: WROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
| TITLE OF INVENTION: WROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
| TITLE OF INVENTION: WROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
| TITLE OF INVENTION WROPER: 05/09/814,292
| CURRENT FILING DATE: 2001-10-12
| PRIOR FILING DATE: 2000-03-24
| NUMBER OF SEQ ID NOS: 46
| SOFTWARE FEASTEQ FOR Windows Version 4.0
| SEQ ID NO 3
| LINGTH: 307
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Patent No. US200201336707A1
BELEAL INFORMATION:
APPLICANT: Yu, D.
APPLICANT: Henderson, D.R.
APPLICANT: Schuur, B.R.
TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
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241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300
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100.0%; Pred. No. 2.3e-91;
tive 0; Mismatches 0;
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Best Local Similarity 100.'
Matches 307; Conservative
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US-09-814-292-3
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Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TIGCCIAAAGCGCAGACGCGCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC
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Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels
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120

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180

240 240

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61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
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                                                                                                                                                                                                                                  Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Description of Unknown Organism: Unknown
US-09-151-376-61
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS FILE REFERENCE: 34802000221 CURRENT APPLICATION NUMBER: US/09/151,376 CURRENT FILING DATE: 1998-09-10 EARLIER APPLICATION NUMBER: 08/669,753 EARLIER FILING DATE: 1996-06-26 EARLIER FILING DATE: 1995-06-27 NUMBER: OR 495,034 EARLIER FILING DATE: 1995-06-27 SOFTWARE: PAPELICATION NUMBER: 08/495,034 SAFLIER FILING DATE: 1995-06-27 SOFTWARE: PALENTH: 307 LENGTH: 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 307; DB 3;
100.0%; Pred. No. 2.3e-91;
Five 0: Mismatches 0;
                                                                                                                                                                                                                           100.0%; Score 307; DB 3;
100.0%; Pred. No. 2.3e-91;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 61, Application US/09151376; Publication No. US2030044383A1; GENERAL INFORMATION: APPLICANT: Henderson, D.R.
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 307
                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 307; Conservative
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Best Local Similarity 100.
Matches 307; Conservative
                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 TGATTAA 307
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                                                                                                              ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(304)
US-09-151-376-10
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ORGANISM: Unknown
FEATURE:
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SOFTWARE: PatentIn Release #1.0, Version #1.30
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Publication No. US20030044383A1
GENERAL INFORMATION:
APPLICANT: Henderson, D.R.
TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
FILE REPERBNCE: 34802200021
CURRENT FILING DATE: 1996-09-10
SARLIER FILING DATE: 1996-06-26
FARLIER FILING DATE: 1996-06-26
SARLIER FILING DATE: 1995-06-27
SARLIER APPLICATION NUMBER: 08/699,753
EARLIER FILING DATE: 1995-06-26
SARLIER FILING DATE: 1995-06-27
NUMBER OF SEQ ID NOS: 71
                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/033,428
FILING DATE: -Unknown:
ATORNEY/AGENT INFORMATION:
NAME: POLIZZI, CATHERINE M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-30004.00
TELECOMMUNICATION INFORMATION:
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100.0%; Pred. No. 2.3e-91;
vative 0; Mismatches 0;
SOFTWAKE: CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 2..304
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 413-5600
TELEPAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ 1D NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                  FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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Matches 307; Conservative
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Best Local Similarity
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US-09-151-376-10
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RESULT 8
US-09-814-351-17
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                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/08814357

Publication No. US20030068307A1

GENERAL INFORMATION:

APPLICANT: Chen, Yu

APPLICANT: Chen, Yu

APPLICANT: Henderson, Daniel R.

TITLE OF INVENTION: METHODS OF TREATING NEOFLASIA

TITLE OF INVENTION: METHODS OF TREATING NEOFLASIA

TITLE OF INVENTION: METHODS OF TREATING NEOFLASIA

TITLE OF INVENTION: MITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,

TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION

FILE REFERENCE: 348022001600

CURRENT APPLICATION NUMBER: 0S/09/814,357

CURRENT FILING DATE: 2001-01-15

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 35

SEQ ID NO 17

LENGTH: 307
                                                                                                  TTGCCTAAAGCGCAGACGCCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 307; Conservative
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APPLICANT: Lamparski, Henry
Schuur, Eric
Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
THEREOF
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                                                                                                APPLICANT: Li, Yuanhao
APPLICANT: Li, Yuanhao
APPLICANT: Li, Yuanhao
APPLICANT: Li, Yuanhao
TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
FILE REFERENCE: 348022001700
CURRENT APPLICATION NUMBER: US/09/814,351
CURRENT PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/192,156
PRIOR PILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 307
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100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Nucleotide sequence for ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 19, Application US/10045116
; Publication No. US20030026792A1
; GENERAL_INFORMATION:
; Sequence 17, Application US/09814351; Publication No. US2030148520A1; GENERAL INFORMATION: APPLICANT: Yu, De-Chao
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 TGATTAA 307
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61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
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                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEE FOR Windows
SOFTWARE: FASTSEE FOR WINDOWS
TOTAL APPLICATION DATA:
APPLICATION NUMBER: US/10/222,479
FILING DATE: 16-Aug-2002
CLASSIFICATION: CURNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: CATherine, Polizzi M
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-20007.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEPRAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 307; DB 5;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/614,495
FILING DATE: 11-Jul-2000
APPLICATION NUMBER: 09/033,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Coding Sequence
LOCATION: 2...304
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEG ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
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                                 NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGATTAN 307
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Publication No. US20030091538A1
GENERAL INFORMATION:
APPLICANT: Yu, De Chao
Schuur, Eric
Henderson, Daniel
TITLE OF INVENTION: ADENOVITEUS VECTORS SPECIFIC
FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGCCTAAAGCGCAGACGCGCCAGACCCCCATCTATAGGCCTATCATTGTTGTTCAACCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AACAICTGCCCTAAATTTACCCCCAAGTTCATGCCTTTGTCAATGACTGGGGGGAGCTTGGA 120
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COMPUTER READABLE FORM:

MEDLUM TYPE: Floppy disk

MEDLUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARR: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/045,116

FILING DATE: 23-Cct-2001

CLASSIFCATION ATMA:

APPLICATION NUMBER: US/09/033,555A

FILING DATE: US/09/033,555A

FILING DATE: CATHERINE M.

REGISTRATION NUMBER: 40,130

REGISTRATION NUMBER: 40,130

REGISTRATION NUMBER: 34802-30005.00
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; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-045-116-19
                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 433-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Matches 307; Conservative
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Indels

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CATGTGGTGGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATTATGTGGCTTATTTG 180
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                                                                                                                                    GENERAL INFURGATION:
GENERAL INFURGATION:
APPLICANT: Schuur, E.R.
TITLE OF INVENTURON: TISSUE SPECIFIC VIRAL VECTORS
FILE REFERENCE: 348022000221
CURRENT APPLICATION NUMBER: US/10/139,089
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 08/69,753
PRIOR APPLICATION NUMBER: 08/69,753
PRIOR FILING DATE: 1996-06-26
PRIOR APPLICATION NUMBER: 09/509,591
PRIOR APPLICATION NUMBER: 09/509,591
PRIOR APPLICATION NUMBER: 09/509,591
PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1998-03-02
PRIOR APPLICATION NUMBER: 09/033,428
PRIOR APPLICATION NUMBER: 09/033,428
PRIOR APPLICATION NUMBER: 09/033,555
PRIOR APPLICATION NUMBER: 09/033,555
PRIOR PILING DATE: 1997-03-03
PRIOR APPLICATION NUMBER: 09/033,555
PRIOR APPLICATION NUMBER: 09/033,333
PRIOR APPLICATION NUMBER: 09/033,333
PRIOR APPLICATION NUMBER: 09/033,333
PRIOR APPLICATION NUMBER: 60/039,762
PRIOR APPLICATION NUMBER: 60/039,762
PRIOR APPLICATION NUMBER: 60/039,762
PRIOR PILING DATE: 1998-03-02
PRIOR PILING DATE: 1999-03-03
PRIOR PILING DATE: 1998-03-05
PRIOR PILING DATE: 1999-03-03
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100.0%; Pred. No. 2.3e-91;
iive 0; Mismatches 0;
RESULT 11
US-10-139-089-10
is Sequence 10, Application US/10139089
is Publication No. US20030152553A1
igeneral Information:
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Matches 307, Conservative
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ORGANISM: Homo sapiens
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TGATTAA 307
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, LOCATION: (2)..(304)
US-10-139-089-10
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RESULT 12

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61 ACATCTGCCCTAAATTTACCCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
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                                                                                                                                   APPLICANT: SCHUUT, B.R.

TITLE OF INVENTION: TISSUB SPECIFIC VIRAL VECTORS
FILE REFERENCE: 349622000221
CURRENT PAPLICATION NUMBER: US/10/139,089
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 08/669,753
PRIOR PILING DATE: 1996-06-26
PRIOR FILING DATE: 1995-06-27
PRIOR FILING DATE: 1995-06-27
PRIOR FILING DATE: 1998-03-02
PRIOR PILING DATE: 1998-03-02
PRIOR PLING DATE: 1998-03-02
PRIOR PLING DATE: 1998-03-02
PRIOR PLING DATE: 1998-03-02
PRIOR FILING DATE: 1998-03-02
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PRIOR PLING DATE: 1999-03
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100.0%; Score 307; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0;
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US-10-691-045-17
Sequence 17, Application US/10691045
Publication No. US20040146489A1
Sequence 61, Application US/10139089
Publication No. US20030152553A1
GENERAL INFORMATION:
APPLICANT: Henderson, D.R.
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ORGANISM: Unknown
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Query Match
Best Local Similarity 100.0
Matches 307; Conservative
SEQ ID NO 10
LENGTH: 307
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                       ; NAME/KEY: CDS
; LOCATION: (2)..(304)
US-10-822-873-10
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ORGANISM: Unknown
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                                                                                        FEATURE:
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                                 APPLICANT: Li, Yuanhao
APPLICANT: Li, Yuanhao
APPLICANT: Li, Yuanhao
APPLICANT: Li, Yuanhao
APPLICANT: Henderson, Daniel R.
TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS RIBOSOME ENTRY SITE
FILE REFERENCE: 348022001700
CURRENT APPLICATION NUMBER: US/09/814,351
PRIOR FILING DATE: 2003-10-21
PRIOR FILING DATE: 2001-03-21
PRIOR PAPLICATION NUMBER: 60/192,156
PRIOR PAPLICATION NUMBER: 60/192,156
PRIOR PAPLING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PREESEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 307
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Sequence 10, Application US/10822873

Publication No. US20040241857A1

GENERAL INFORMATION:

APPLICANT: Henderson, D.R.

APPLICANT: Schuur, E.R.

TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS

FILE REFERENCE: ECLL-004CON2

CURRENT APPLICATION NUMBER: US/10/822,873

CURRENT APPLICATION NUMBER: 09/732,169

PRIOR APPLICATION NUMBER: 09/132,169

PRIOR PELING DATE: 1998-09-10

PRIOR FILING DATE: 1998-09-10

PRIOR FILING DATE: 1996-06-26

PRIOR FILING DATE: 1996-06-26

PRIOR FILING DATE: 1995-06-27

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Nucleotide sequence for ADP US-10-691-045-17
                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 307; Conservative
GENERAL INFORMATION:
APPLICANT: Yu, De-Chao
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100.0%; Score 307; DB 8; Length 307; 100.0%; Pred. No. 2.3e-91; ive 0; Mismatches 0; Indels
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Sequence 61, Application US/10822873

Sequence 61, Application US/10822873

Sequence 61, Application US/1082873

GENERAL INFORMATION:

APPLICANT: Benderson, D.R.

TITLE OF INVERTION:

TITLE REPERENCE: CELL-004-00-13

CURRENT APPLICATION NUMBER: US/10/822,873

CURRENT APPLICATION NUMBER: 09/132,169

PRIOR PILING DATE: 2000-12-06

PRIOR PILING DATE: 1998-09-10

PRIOR FILING DATE: 1998-09-10

PRIOR FILING DATE: 1996-06-26

PRIOR PILING DATE: 1996-06-26

PRIOR PILING DATE: 1996-06-26

PRIOR FILING DATE: 1995-06-27

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 61

LENGTH: 307
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1 GATGACCGCCTCAACCATCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT 60	61 AACATCTGCCCTAAATTTACCCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
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61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGGGC	61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGGCGAGCTTGGA 120	121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGCCTTATTATTATTATGTGGCTTATTTG 180

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²⁴¹ ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTTTTTTACAGTA 300 241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300

³⁰¹ TGATTAA 307 ||||||| 301 TGATTAA 307

Search completed: January 20, 2006, 21:23:53 Job time : 806 secs

7472, Ap 17, Appl

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence 17565, A Sequence 12504, A Sequence 71369, A Sequence 113176,

Sequence 216, App Sequence 12, Appl Sequence 37, Appl

Sequence 12371, A

13845,

Sequence

-09-596-002-37

ALIGNMENTS

```
APPLICANT: Yu, De Chao
APPLICANT: Yu, De Chao
APPLICANT: Schuur, Eric
APPLICANT: Schuur, Eric
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
WUMBER OF SEQUENCES: 22
CORRESPONDENCES: ADDRESS:
ADDRESSES: MORRISON & FORSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                            US-09-952-060-28
US-10-131-827-7472
US-09-007-005-17
US-09-244-796-17
US-09-949-016-17565
US-09-949-016-17369
US-09-949-016-13369
US-09-949-016-113176
US-09-949-016-113176
US-09-949-016-113176
US-09-949-016-113176
US-09-724-394A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Atto
STATE: CA
COUNTRY: UGA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM Compatible
COPRATING SYSTEM: Windows
SOFTWARE: PastENG for Windows
SOFTWARE: PastENG for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033,333
                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-016-13845
US-09-949-016-12371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFFLING DATE: 05/05/03/333
FILING DATE: 02/05/03/333
FILING DATE: 02-MAR-1998
CLASSIFICATION OF A.:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-20007.00
TELECOMMUNICATION INFORMATION:
TELECHONE: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/09033333 Patent No. 6197293 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELERAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                           35935
35935
35978
36620
37474
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Sequence 1, A
Sequence 1, A
Sequence 43,
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Sequence 10,
Sequence 61,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Issued Patents NA:*
| cgn2 6/ptodata/1/ina/1 COMB.seq:*
| cgn2 6/ptodata/1/ina/5 COMB.seq:*
| cgn2 6/ptodata/1/ina/6A COMB.seq:*
| cgn2 6/ptodata/1/ina/6B COMB.seq:*
| cgn2 6/ptodata/1/ina/H COMB.seq:*
| cgn2 6/ptodata/1/ina/PP COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-033-33-21
US-09-033-428-22
US-09-033-556-9
US-09-614-495-21
US-09-151-376-10
US-09-151-376-10
US-09-151-376-11
US-09-151-376-11
US-09-161-351-17
US-09-17-35-32-33
US-09-111-911-5
US-09-17-35-33-33-33
US-09-563-8693-3
US-09-563-8693-3
US-09-563-8693-3
US-09-563-8693-3
US-09-563-8693-3
US-09-563-8693-3
US-08-563-8693-3
US-08-563-8693-3
US-08-735-609-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     OM nucleic - nucleic search, using sw model
                                                                                                                                             January 20, 2006, 19:14:55
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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307
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Match Length DB
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                                                                                                                                                                                                                                                                                                                  Scoring table:
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303.8
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                                                                                                                                                                                                                                                                                                                                                                                Searched:
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No.
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STRANDEDNESS: double
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Bacter No. 625462

GENERAL INFORMATION:
APPLICANT: Little, Andrew
APPLICANT: Little, Henry
APPLICANT: Lomparski, Henry
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
TITLE OF INVENTION: EXRESSING APPA-FETOPROTEIN AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSED: MORRISON & FORESTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                             CATGIGGTGGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATTATGTGGGCTTATTTG 180
                                                                                                                                                                                                                                                                                                                                                                                TTGCCTAAAGCGCAGACGCCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC 240
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                                                                                                                                                                                                                                              61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
                                                                                                                                                                                                                                                                                                       CATGTGGTGGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATTATGTGGCTTATTTG 180
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                                                                                                                                                                        1 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACACTGCTACCGGACT 60
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                                                                        Length 307;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033,428
FILING DATE:
                                                                        100.0%; Score 307; DB 3;
100.0%; Pred. No. 1.6e-97;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILLING DALES
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: POLIZZI, CATHERINE M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-30004.00
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 813-5600
TELEFAX: (415) 8494-0792
TELEFAX: (415) 494-0792
TELEFAX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
                                                                            Query Match
Best Local Similarity 100.
Matches 307; Conservative
; LOCATION: 2...304
; OTHER INFORMATION:
US-09-033-333-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGATTAA 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-033-428-22
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APPLICANT: Henderson, Daniel R.
APPLICANT: Henderson, Daniel R.
APPLICANT: Yu, De Chao
APPLICANT: Yu, De Chao
TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
TITLE OF INVENTION: OF USING SAME
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOREISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
IF 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
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                                                                                                                                                                                                                                                                                                                                                                       61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CATGIGGIGGITITICCATAGCGCITATGITIGITIGCCITATTATTATGIGGCTTATTIG 180
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                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033,556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-20010.00
TELECOMMULICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEPHONE: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09033556; Patent No. 6432700; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
; TOPOLOGY: linear; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..304
US-09-033-428-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 TGATTAA 307
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Sequence 22, Application US/0989883
Patent No. 6585968
GENERAL INFORMATION:
APPLICANT: Little, Andrew
Lamparski, Henry
Schuur, Eric
Henderson, Daniel
TITLE OF INVENTION: ADANIELS APPRAFETOPROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CATGLGGTGGTTTTCCATAGCGCTTATGTTTGCTTTGCCTTATTATTATTATGGCCTTATTTG 180
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                 NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-20007.00
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-494-0792
TELEFAX: 650-494-0792
INFORMATION POR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 307; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0;
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-614-495-21
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STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
  INFORMATION
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Coding (LOCATION: 2...304) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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  ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                   FEATURE
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US-09-898-883-22
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US-09-614-495-21
Sequence 21, Application US/09614495
Sequence 21, Application US/09614495
Sequence 21, Declar
General Information:
Henderson, Daniel
Henderson, Daniel
Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
HERBOPE
TITLE OF INVENTION: ADENOVIRUS AND METHODS OF USE
TITLE OF INVENTION: ADENOVIRUS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
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                                                                                                                                                                                                                                                                                                             Length 307;
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBW Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             100.0%; Score 307; DB 3;
100.0%; Pred. No. 1.6e-97;
tive 0; Mismatches 0;
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FILING DATE: 11-Jul-2000
CLASSIFICATION: UDKNOWN:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/033,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
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                                                                                                                                                                                     NAME/KEY: Coding Sequence
LOCATION: 2...304
CTHER INFORMATION:
US-09-033-556-9
            INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 307; Conservative
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SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09151376
Sequence INFORMATION:
GENERAL INFORMATION:
APPLICANT: Benderson, D.R.
APPLICANT: Benderson, TISSUB SPECIFIC VIRAL VECTORS:
ITLE OF INVENTION: TISSUB SPECIFIC VIRAL VECTORS:
FILE REPERENCE: 34802200021
CURRENT FILING DATE: 1996-06-100-10
EARLIER FILING DATE: 1996-06-26
EARLIER FILING DATE: 1996-06-26
EARLIER PILING DATE: 1995-06-27
EARLIER PILING DATE: 1995-06-27
NUMBER OF SEQ ID NOS: 71
                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: POLIZZI, CATHERINE M.
REGISCRATION NUBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-30004.00
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 813-5600
TELEPAX: (415) 494-0792
TELEPX: 706141 MESNFOERS SFO
INFORMATION FOR SEQ ID NO: 22:
                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/033,428
FILING DATE: <Unknown>
               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,883
FILING DATE: 02-011-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 2..304
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                          LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 307; Conservative
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TGATTAA 307
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100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                    Length 307;
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; Sequence 61, Application US/09151376
; Patent No. 6676935
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.;
; APPLICANT: Schuur, E.R.;
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS;
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS;
; TITLE OF INVENTION: 1980-021
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 08/659,753
; EARLIER APPLICATION NUMBER: 08/659,753
; EARLIER APPLICATION NUMBER: 08/495,034
; EARLIER PILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 51
; SEQ ID NO 61
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                                                                                                                                                                                                                                                    Score 307; DB 3;
Pred. No. 1.6e-97;
                                                                                                                                                                                                                                                 Query Match
100.0%; Score 307; D
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 307; Conservative 0; Mismatches
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 307
                                                                        TYPE: DNA
CRGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(304)
US-09-151-376-10
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ORGANISM: Unknown
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301 TGATTAA 307
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US-09-392-822A-7
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Patent No. 6692736

GENERAL INFORMATION:
APPLICANT: Yu, De-Chao
APPLICANT: Yu, De-Chao
APPLICANT: Li, Yuanhao
APPLICANT: Li, Yuanhao
TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
FILE REFERENCE: 348022001700
CURRENT APPLICATION NUMBER: 60/192,156
PRIOR PILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASESEQ for Windows Version 4.0
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100.0%; Score 307; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0;
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US-09-814-351-17
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LENGTH: 307
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Sequence 3, Application US/09814292
| Sequence 3, Application US/09814292
| Sequence 3, Application US/09814292
| Patent No. 685258
| GENERAL INPORMATION:
| APPLICANT: Thang, Hong
| APPLICANT: Abriderson, Daniel R.
| TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN
| TITLE OF INVENTION: HEADSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING
| TITLE OF INVENTION: WROTHORN: WROTHORN SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
| TITLE OF INVENTION: WROTHORN: BETONG OF USE THEREOF
| TITLE OF INVENTION: WROTHORN: BETONG OF USE THEREOF
| FILE REFERENCE: 346022001500
| CURRENT APPLICATION NUMBER: 60/191,861
| PRIOR FILING DATE: 2000-03-24
| NUMBER OF SEQ ID NOS: 46
| SOFTWARE: PASESEQ for Windows Version 4.0
| SEQ ID NO 3
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Sequence 7, Application US/0939282A

Patent No. 6900049

GENERAL INFORMATION:
APPLICANT: Yu, De Chao
TITLE OF INVENTION: Adenovirus Vectors Containing Cell
TITLE OF INVENTION: Status-Specific Response Blements and Methods of Use Thereof
TITLE OF INVENTION: Status-Specific Response Blements and Methods of Use Thereof
TITLE REFERENCE: CELL-014; 122.1

CURRENT APPLICATION NUMBER: US/09/392,822A

CURRENT FILING DATE: 1998-09-09

PRIOR FILING DATE: 1998-09-10

PRIOR FILING DATE: 1999-09-09
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100.0%; Score 307; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0;
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US-09-875-228-4
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Patent No. 6911200

GENERAL INFORMATION:
APPLICANT: Turne De-Chao
TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA
TITLE OF INVENTION: MITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,
TITLE OF INVENTION: MITH COMBINATION
TITLE OF INVENTION: MITH COMBINATION
FILE REFERENCE: 348022001600
CURRENT APPLICATION NUMBER: 05/192,015
PRIOR FILING DATE: 2001-01-15
NUMBER OF SEQ ID NOS: 35
SORTHARE: FREESEQ for Windows Version 4.0
SEQ ID NO 17
MADEL NO 17
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100.0%; Pred. No. 1.6e-97;
tive 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7
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ORGANISM: Artificial Sequence
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Matches 307; Conservative
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                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (20)...(304)
US-09-392-822A-7
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TGATTAA 307
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Best Local Similarity
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                                                                               TYPE: DNA
ORGANISM: Adenovirus
                                                             LENGIH: 307
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APPLICANT: Yu, D.
APPLICANT: Yu, D.
APPLICANT: Yu, D.
APPLICANT: Yu, D.
APPLICANT: Schuur, E.R.
TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE
TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE
TITLE OF INVENTION: A HUMAN GLANDULAR COMPRISING THE
TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF
TITLE OF INVENTION WHORER: US/09/875,228
CURRENT APPLICATION NUMBER: 00/127,834
PRIOR FILING DATE: 1998-03
PRIOR PILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: 60/076,545
PRIOR FILING DATE: 1999-03-02
PRIOR FILING DATE: 1999-03-02
PRIOR PILING DATE: 1999-03-05
PRIOR PILING DATE: 1997-08-04
SEQ ID NO 4
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                                                                                                                            CATGTGGGTGGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATATTATTATGTGGCTTATTTG
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                                                61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA
                                                                                                                                                                                                   181 TIGCCTAAAGGGCAGACGCCAGACCCCCCATCTATAGGCCTATCATGTGTCCCCCC
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61 AACATCTGCCCTAAATTTACCCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA
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100.0%; Score 307; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0;
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; Patent No. 6916918
; GENERAL INFORMATION:
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LOCATION: (2)..(307)
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US-09-562-930-11
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US-09-111-911-5/c
; Sequence 5, Application US/09111911
; Sequence 5, Application US/09111911
; Patent No. 681402
; GENERAL INFORMATION:
; APPLICANT: Wold, William S.M.
; TITLE OF INFORMATION:
; FILE REFERENCE: 1615-5-56
; CURRENT APPLICATION NUMBER: US/09/111,911
; CURRENT FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 5
; COFFWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29467 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT
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100.0%; Score 307; DB 3; Length 35937;
Best Local Similarity 100.0%; Pred. No. 1.9e-96;
Matches 307; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                     APPLICANT: Hearing, Patrick
APPLICANT: Bahou, Wadie
APPLICANT: Sandalon, Ziv
APPLICANT: Sandalon, Ziv
APPLICANT: Gardenko, Dmitri
TITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONYB-04970
CURRENT APPLICATION NUMBER: US/09/782,378A
CURRENT FILING DATE: 2001-02-12
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human adeno-associated virus 2
US-09-782-378A-3
                                                                                                                                                    Sequence 3, Application US/09782378A Patent No. 6916635 GENERAL INFORMATION:
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US-09-782-378A-3
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                                                                                                                                          Length 34427;
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Plasm
OTHER INFORMATION: Combining E.coli and Adenovirus Sequences
                                                                                                                                                                              Indels
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99.3%; Pred. No. 2.5e-95;
tive 0; Mismatches 2;
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Pred. No. 1.7e-57;
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; Patent No. 6835812
                                                                                                                                        Query Match
Best Local Similarity 99.33
Matches 305, Conservative
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Search completed: January 20, 2006, 21:10:15 Job time : 147 secs

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AAV53632
AAX07371
ADA09839
ADW28319
ADF60698
ADF60698
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AAC89170
ADW11287
                                       AAA09092
AAA14723
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AAC85018
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January 20, 2006, 17:03:15; Search time 472 Seconds (without alignments) 4334.874 Million cell updates/sec
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    GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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                            - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                              seq length: 0
seq length: 200000000
                                                             US-10-822-873-10
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           Copyright
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Title: Perfect score:

Sequence:

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Run

Scoring table:

Searched:

Aag68003 Ad2/-ORF6
Aav53622 Adenoviru
Adav2319 Adenoviru
Adav2319 Nucleotid
Ad60698 Ad6 genom
Ad800148 Human ade
Aaa09092 AdMMTV-be
Aaa1723 Nucleotid
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Aaa132 Partial 8
Aaa1803 Nucleotid
Aaa9332 Partial 8
Aaa93332 Partial 8
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## ALIGNMENTS

RESULT 1

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB Maximum DB

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ANA OFFI	ID ANVA7675 standard: DNA: 307 BP.		LE CENTRAL CA		DT 07-DEC-1998 (first entry)	XX	DE Adenovirus death protein gene.	×	KW Adenovirus death protein: ADP: vector: hepatoma: cancer:			OS Mastadenovirus.		FH Kev Location/Qualifiers		FT /*tag= a		PN WO9839465-A2.	PD 11-SEP-1998.		PF 03-MAR-1998; 98WO-US004084.		03-MAR-1997;	PR 02-MAR-1998; 98US-00033428.		PA (CALY-) CALYDON INC.		PI Little AS, Lamparski HG, Henderson DR, Schuur BR;		DR WPI; 1998-495861/42.	DR P-PSDB; AAW61197.	XX	PT New adenovirus vector, for treating cancers - comprising an adenovirus	PT gene under the transcriptional control of an alpha fetoprotein			PS Claim 31; Page 74; 102pp; English.	
3. denesem2000s.*	4: genesedn2001as:*	5: genesedn2001bs:*		/: genesednz00zbs:*	9: geneseqn2003bs:*	10: geneseqn2003cs:*	11: geneseqn2003ds:*				Pred. No. is the number of results predicted by chance to have a		and is derived by analysis of the total score distribution.		SUMMARIES	***	lt Query	o. Score Match Length DB ID Description	100.0 307 2 AAV47675 Aav47675	100.0 307 2 AAV52966 Aav52966	100.0 307 2 AAV57354 Aav57354	307 100.0 307 2 AAX24756 Aax24756	. 307 100.0 307 3 AAZ99937 Aaz99937	307 100.0 307 4 AAI70186 . Aai70	307 100.0 307 5 AAH43535	307 100.0 307 6 ABK99587 Abk99	307 100.0 307 8 ACD07312 Acd07	307 100.0 307 12 ADI36397 Adi3	100.0 307 12 ADI36417	307 100.0 307 14 ADV21029	307 100.0 307 14 ADV20978	307 100.0 307 14 ADW47774	307 100.0 917 14 ADW28317		307 100.0 35209 14 ADW28315	100.0 35937 6 ABS69881 Abs69	19 307 100.0 35937 9 ACC70007 ACC70007 Nucleotid	

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Result ò

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New adenovirus vectors, particularly for cancer therapy - comprising adenovirus gene under transcriptional control of carcinoembryonic antigen transcriptional regulatory element.
                                                                                                                                                                                                                                                                                  This is the coding region of the adenovirus death protein (ADP, see AAW78902). It can be obtained by PCR amplification (see also AAV52945-46). Claimed replication-competent adenovirus (Ad) vectors comprise an Ad gene under transcriptional control of a CEA-TRE. The vectors can be used to detect and monitor samples for the presence of cells that allow a CEA-TRE to function, and to selectively kill such cells, especially malignant cells. Octors containing an ADP gene may be more potent than vectors dosage requirement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 307; DB 2; Length 307; Pred. No. 2.4e-94; 0; Mismatches 0; Indels
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                                                                           Schuur ER;
                                                                                                                                                                                                                                                      Disclosure; Page 67-68; 95pp; English
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                                      (CALY-) CALYDON INC
                                                                                                                                   P-PSDB; AAW78902
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02-MAR-1998;
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                                  AW61197) of adenovirue type 2. The ADP coding sequence (with or without the Y leader) can be introduced into an adenoviral genome, e.g. in the E3 or E4 region. Inclusion of such a coding sequence in an adenoviral vector significantly enhances the extent of cytocoxicity, cell killing and virus production. The invention provides replication-competent adenovirus vectors which preferentially replicate in cells that express alphatetoprotein (AFP), particularly heptoma cells. The vectors comprise at least one adenovirus gene, preferably a gene that contributes to cytocoxicity, under the transcriptional control of an AFP transcription conferring selective cytotoxicity to AFP-expressing cells, especially cancer cells. (Updated on 27-AUG-2003 to correct OS field.)
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                      nucleotide sequence codes for adenovirus death protein (ADP, see
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                                                                                                                                                                                                                                                                                                                This is the coding region of the adenovirus death protein (ADP, see AAW75787). It can be obtained by PCR amplification (see also AAV57350-51). Claimed replication-competent adenovirus (Ad) vectors comprise an Adgene under transcriptional control of a probasin transcriptional response element (PB-TRE, see AAV57334). The vector can be used for detecting calls that allow a PB-TRE to function, especially cells expressing an androgen receptor, such as prostate cells. They can be used to confer selective toxicity to such cells. In particular, the vectors can be used for treating cancers such as prostate cancer. Ad vectors can be used for treating cancers such as prostate cancer. Ad vectors can be used for treating cancers such as prostate cancer. Ad vectors can be used fective treatment and/or a lower dosage requirement. An Ad vector has been constructed that contains the ADP gene under control of PB-TRE. Cytcoxicity was demonstrated toward LNCaP (prostate carcinoma) cells
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                                                                                                                                                                                                                                          New adenovirus vectors, particularly for cancer therapy - comprising an adenovirus gene under transcriptional control of a probasin transcriptional regulatory element.
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                                                                                                                                                                                                                                                                                             Disclosure, Page 96; 117pp; English.
                                                                                                                                                                             Schuur ER,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                          glandular kallikrein-1; hGK-1; hKLK2; human; prostate cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                          2. .309
/*tag= a
/product= "adenovirus death protein"
                                                                                                DNA encoding adenovirus death protein.
                                                                                                                                                                                            therapy; adenovirus death protein; as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 165; 179pp; English
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schuur ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0076545P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US016312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0054523P
                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 307; Conservative
                                                                                                                                                                                                                                                              Human adenovirus type 2.
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herdenson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-153804/13.
P-PSDB; AAW98003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CALY-) CALYDON INC
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180

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61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
                           121 CATGIGGIGGITTICCADAGCGCITATGITIGITIGCCTATIATATGIGGCTTAITG
                                                                                                                                                                                                                                                                                                                                              11-SEP-2003
07-JAN-2002
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                                                                                                                                                                                                                                                                                                                     AAI70186;
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                                                                                                                                                                                                                                                                RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes an adenoviral death protein, which is used to construct the vectors of the invention. The specification describes adenoviral vectors which comprise an adenoviral gene under transcriptional control of a call status specific transcriptional regulatory element (TRE). The TRE is preferably one that is essential for adenovirus propagation. The adenovirus vectors may be used for the treatment of a range of tumours such as lung, stomach, breast, colon and rectum, and uterine and cervix cancers
                 300
                               241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300
                  ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adenovirus vectors comprising cell-status specific response elements useful in gene therapy protocols for the treatment of cancers.
                                                                                                                                                                                                                                                                              adenoviral vector, adenovirus gene; transcriptional control;
transcriptional regulatory element; TRB; adenoviral propagation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 307; DB 3;
100.0%; Pred. No. 2.4e-94;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "death protein"
                                                                                                                                                                                                                                                     DNA encoding an adenoviral death protein.
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 2. .307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 9; 79pp; English
                                                                                                                                                                   AAZ99937 standard; DNA; 307 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US020718
                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                           death protein; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 307; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Henderson DR;
                                                                       TGATTAA 307
                                                                                                  TGATTAA 307
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                                                                                                                                                                                                                                                                                                                                      Mastadenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200015820-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-SEP-1999;
                                                                                                                                                                                                                          25-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000
                                                                                                                                                                                                AAZ99937;
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The present sequence is that of the coding region of the adenovirus death protein. The sequence was obtained by PCR amplification and used in the construction of adenoviral vectors in which ADP expression was under the control of a urothelial cell-specific transcriptional regulatory element (TRE) derived from the human uroplakin II gene 5' flanking region (see AAI70144). This is an example of adenoviral vectors of the invention. Such vectors comprise a gene, preferably an adenovirus gene, under transcriptional control of a urothelial cell-specific cytotoxicity, and are used for the specific, targeted gene therapy of bladder cancer. (Updated on II-SEP-2003 to standardise OS field)
                                                                       240
                                                                                                           300
121 CATCTGGTGGTTTTCCATAGCGCTTATGTTTGCCTTATTATTATGTGGCTTATTTG 180
                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adenovirus death protein; uroplakin II; vector;
transcriptional regulatory element; TRE; urothelial cell; bladder cancer;
                                                                                                                                            241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human urothelial cell specific uroplakin transcriptional regulatory sequences, useful for producing adenoviral vectors which can be used to confer selective cytotoxicity to target cells, especially bladder cancer
                                                                    181 TTGCCTAAAGCGCAGACGCCAGACCCCCCATCTATGAGCCTATCATTGTGCTCAACCC
                                      181 TIGCCIAAAGCGCAGACGCGCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC
                                                                                                           241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
2. .307
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Adenovirus death protein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang H, Henderson DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2001; 2001WO-US009224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-2000; 2000US-0191861P.
                                                                                                                                                                                                                                                                                                            AAI70186 standard; DNA; 307
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human adenovirus type 2.
                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639229/73.
P-PSDB; AAM50206.
                                                                                                                                                                                    301 TGATTAA 307
                                                                                                                                                                                                            301 TGATTAA 307
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Gaps

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Indels

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9

61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120

GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACAACACCACTGCTACCGGACT 60 1 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT

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This sequence encodes adenoviral ADP. This coding sequence may be used in the replication-competent adenoviral vector (A) of the invention which contains two genes (G1, G2) that are co-transcribed as a single mRNA and under control of a heterologous, target cell-specific transcriptional regulatory element (TRE). G2 has a mutation in, or deletion of, its endogenous promoter and is controlled from an internal ribosome entry atte (IRES). The ADP coding sequence may be used as G1 or G2. (A) has greater specificity for a target cell than a similar vector in which TRE is operably linked to a gene and which lacks an IRES. (A) are used to modify the genotype of target cells, optionally in vitro with subsequent return of altered cells to the host and where G2 is a cytocoxic gene, to confer selective cytocoxicity to target cells, especially for killing cancer cells. ADP displays a cytotoxic, particularly cell lysis, function. Also (A) are used for diagnosis and monitoring, e.g. detection of bladder cancer cells. The target cell-specific TRE ensures that (A) has better targeting specificity, with minimal replication in non-target cells, so a runaway infection is prevented but production of adenoviral proteins in target cells activates and/or stimulates the immune response than two identical control elements) eliminates the risk of homologous recombination and may provide enough extra space for an additional control elements) eliminates the risk of homologous recombination and may provide enough extra space for an additional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AACATCTGCCCTAAATTTACCCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AACATCTGCCCTAAATTTACCCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATTATGTGGCTTATTTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATTATGTGGCTTATTTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TTGCCTAAAGCGCAGACGCCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adenovirus; transcriptional regulatory element; TRB; prostate; liver; breast cancer; colon cancer; antitumour; gene; ds; probasin; PB; human; rat; carcinoembryonic antigen; prostate-specific antigen; ADP; adenovirus death protein; glandular kallikrein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GATGACCGGCTCAACCATCGCGCCCCACAACGGACTATCGCAACACCCACTGCTACCGGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCCACTGCTACCGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGCCTAAAGCGCAGACGCCAGACCCCCCCATCTATAGGCCTATCATGTGCTCAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTACAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 307; DB 5; Length 307; 100.0%; Pred. No. 2.4e-94; Live 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding adenovirus death protein (ADP).
Disclosure; Fig 9; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0%; Matches 307; Conservative C
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                                                                                                                                                                                                                                                                                     CATGIGGIGGITITCCATAGCGCTTATGTTTGCCTTATTATTATGTGGCTTATTTG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adenovirus; ADP; replication-competent; adenoviral vector; TRE; transcriptional regulatory element; mutation; deletion; IRES; promoter; internal ribosome entry site; cytotoxic; cancer; bladder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Replication-competent adenoviral vector, useful e.g. for killing cancer cells, contains two genes linked by internal ribosome entry site and controlled by target-specific regulator.
                                                                                                                                                                                       GATGACCGGCTCAACCATCGCGCCCCACAACGGACTATCGCAACACACCACTACCGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA
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                                                                                                                                                               GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACACCACTGCTACCGGACT
                                                                                                                Gaps
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                                                               100.0%; Score 307; DB 4; Length 307; 100.0%; Pred. No. 2.4e-94; ive 0; Mismatches 0; Indels
                      Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
2. .307
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "ADP"
                                                                                        Best Local Similarity 100.0%;
Matches 307; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2001; 2001WO-US009036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unidentified adenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu D, Li Y, Henderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGATTAN 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATTAN 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200173093-A2
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07-JAN-2002
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                                                                                                                                                                                                                                                                                       The invention relates to an adenovirus vector (AV) comprising an AV gene under transcriptional control of a cell type-specific transcriptional regulatory element (TRE) and optionally a first AV gene under control of a first cell type-specific TRE and a second gene under control of second cell type-specific TRE, where the first and second cell type-specific TRE, where the first and second cell type-specific TRE, where the first and second cell type-specific TREs are substantially identical. When the vector is introduced into a cell (e.g. prostate cell, liver cell, breast cancer cell) it allows the cell type-specific TRE to function, resulting in cycotoxicity. The vector is useful for suppressing tumour growth of a target cell. This sequence represents a polynucleotide used in the scope
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                                                                                                                                                                                                  Novel adenovirus vector comprises adenovirus gene under transcriptional control of cell-type specific transcriptional response element for conferring selective toxicity on target cell and for suppressing tumor
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                                                                          98US-00151376
                                                 06-DEC-2000; 2000US-00732169
                                                                                                                                       Henderson DR, Schuur ER;
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nes 307; Conservative
                                                                                                 HENDERSON D R.
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                                                                                                                                                               WPI; 2002-582468,
P-PSDB; ABG69353
 US2002068049-A1
                                                                          10-SEP-1998;
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(revised)

27-OCT-2003

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The present invention relates to adenoviral vectors comprising an adenovirus gene under transcriptional control of a cell type-specific transcriptional response element (TRE). Example TRES given in the specification include human prostate-specific antigen (BSA) TRE, human glandular kallikrein (hKLK) TRE, rat probastin (PB) TRE, human carcinoembryonic antigen (CEA) TRE, and human mucin-like glycoprotein DF3 (MUC1) TRE. The modified adenovirus vector is useful as a vehicle for introducing new genetic capability, particularly associated with cytocoxicity for treating neoplasia. For example, the vector may be used in a target cell to suppress tumour growth, or to kill the target cell. The vector is particularly useful in gene therapy. The present sequence encodes adenovirus death protein (ADP). (Updated on 27-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
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                                                                                               Adenoviral vector; adenovirus gene; transcriptional control; TRE; call type-specific; transcriptional response element; PSA; hKuk; prostate-specific antigen; glandular kallikrein; probastin; PB; carcinoembryonic antigen; CEA; mucin-like glycoprotein DF3; MUC1; cytotoxicity; neoplasia; tumour growth; gene therapy; cytostatic;
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; Pred. No. 2.4e-94;
0; Mismatches 0;
                                                 DNA encoding adenovirus death protein (ADP)
                                                                                                                                                                                                                                  adenovirus death protein; ADP; gene; ds.
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96US-00699753.
97US-0039597P.
97US-0039762P.
97US-0039763P.
98US-00033428.
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07-AUG-2003 (first entry)
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P-PSDB; ABU10308.
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03-MAR-1997
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proliferations other than tumours, such as psoriatic lesions and wound healing. In addition, it is useful for detecting cells where a cell type specific TRE is functional in a blological sample and for treating prostate-associated diseases such as hyperplasts and cancer. As such, these compositions exhibit cytostatic, antipsoriatic and vulnerary activities. This polynucleotide sequence is the human mucin (MUC1) TRE DNA sequence of the invention. NOTE: This sequence is identical to that given as SeqID 10.
                                                                                                                                                                                                                                                                                                                                                                                    121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATTATGTGGCTTATTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ds; gene; human ; prostate; transcriptional response element; TRE; polyethylene elycol; PEG; masking agent; tumour cell growth; proliferation; psoriatic lesion; wound healing; hyperplasia; cancer; cytostatic; antipsoriatic; vulnerary; ADF.
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                                                                                                                                                                         Length 307;
                                                                                                                                                                                                        Indels
                                                                                                                                           Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
                                                                                                                                                                       100.0%; Score 307; DB 12; 100.0%; Pred. No. 2.4e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding the human ADP protein SeqID10.
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/product= "ADP protein"
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26-JUN-1996;
03-MAR-1997;
03-MAR-1997;
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                                                                 240
                                                                                              300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition comprising replication competent adenovirus having adenovirus gene essential for replication under transcriptional control of cell type specific transcriptional response element and masking agent.
                                                                                                                           ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTTTTTTACAGTA 300
   CATGTGGTGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATGTGTGGCTTATTTG 180
                                                                                                                                                                                                                                                                                                                                                                                            ds; mucin; MUCl; human; prostate; transcriptional response element; TRE; polyethylene glycol; PGG; masking agent; tumour cell growth; proliferation; psoriatic lesion; wound healing; hyperplasia; cancer; cytostatic; antipsoriatic; vulnerary; human.
                                                     TTGCCTAAAGCGCAGACGCCCAACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC
                                                                                            ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA
                                TTGCCTAAAGCGCAGACGCGCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC
                                                                                                                                                                                                                                                                                                                                                               Human mucin (MUC1) transcriptional response element DNA SeqID61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schuur ER
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                                                                                                                                                                                                                                                                      BP.
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96US-00669753.
97US-003957P.
97US-0039762P.
98US-0003333.
98US-00033555.
98US-00033555.
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                                                                                                                                                                                                                                                                    ADI36397 standard; DNA; 307
                                                                                                                                                                                                                                                                                                                                (first entry)
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LAMPARSKI H G.
HENDERSON D R.
                                                                                                                                                          TGATTAA 307
                                                                                                                                                                                       TGATTAN 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2003152553-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAR-1997;
03-MAR-1997;
03-MAR-1997;
02-MAR-1998;
02-MAR-1998;
02-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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02-JUN-2000;
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(LAMP/)
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prostate cancer; gene therapy; vaccine; cytostatic; TRE; transcriptional regulatory element; PSE; prostate specific enhancer; PSA; prostate specific antigen; cancer; ds; mucin like glycoprotein DF3; MUC1.

95US-00495034

27-JUN-1995;

13-APR-2004; 2004US-00822873

US2004241857-A1.

02-DEC-2004

Homo sapiens.

26-JUN-1996; 96US-00669753 10-SEP-1998; 98US-00151376 06-DEC-2000; 2000US-00732169

(HEND/) HENDERSON D R.

(SCHU/) SCHUUR B R.

Schuur ER;

Henderson DR,

WPI; 2005-011642/01.

prostate cancer.

Vector; gene transfer; cloning vehicle; genetic engineering;

Human mucin like glycoprotein DF3 (MUC1) TRE DNA

(first entry)

24-FEB-2005

ВР

ADV21029 standard; DNA; 307

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This invention relates to a novel composition that contains a replication competent adenovirus capable of transfecting target host cells.

Specifically, it comprises an adenovirual gene essential for replication (EIA, EIB or EA), which is under the transcriptional control of a prostate specific transcriptional response element (TRE) and polyethylene glycol (PEG) as the masking agent. The present invention describes this composition as useful for suppressing tumour cell growth and for lowering the levels of tumour cell markers. It can also be used for introducing transferations other than tumours, such as positic lestons and wound healing. In addition, it is useful for detecting cells where a cell typespecific TRE is functional in a biological sample and for treating prostate-associated diseases such as hyperplasia and cancer. As such, these compositions exhibit cytostatic, antiposoriatic and vulnerary activities. This polymucleotide sequence is the DNA encoding the human and protein of the invention. NOTE: This sequence is identical to that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition comprising replication competent adenovirus having adenovirus gene essential for replication under transcriptional control of cell type specific transcriptional response element and masking agent.
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                                                                                                                                                                                                                                                                                                                                                                                                              Henderson DR, Schuur ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 10; 115pp; English
02-MAR-1998; 98US-00033333.
02-MAR-1998; 98US-00033428.
02-MAR-1998; 98US-0013555.
10-SEP-1998; 98US-00151376.
02-UUN-2000; 2000US-00509591.
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hes 307; Conservative
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LAMPARSKI H G.
HENDERSON D R.
SCHUUR E R.
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P-PSDB; ADI36347.
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New adenovirus vector comprising an adenovirus early gene essential for propagation under the control of a human prostate specific antigen promoter and a human prostate specific antigen enhancer, for treating

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
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Matches 307; Conservative
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                            ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300
                                                     Vector; gene transfer; cloning vehicle; genetic engineering; prostate cancer; gene therapy; vaccine; cytostatic; prostate-specific antigen; TRS; transecriptional regulatory element; PSB; prostate specific enhancer; PSA; prostate specific antigen; cancer; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New adenovirus vector comprising an adenovirus early gene essential for propagation under the control of a human prostate specific antigen promoter and a human prostate specific antigen enhancer, for treating prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adenovirus death protein (ADP) encoding DNA
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10-SEP-1998; 98US-00151376.
06-DEC-2000; 2000US-00732169.
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The present sequence is the coding sequence for adenovirus death protein (ADP). A claimed replication competent adenovirus vector comprises: an inducible transcriptional transactivator (TT) coding sequence under the transcriptional control of a cell type-specific TRE (CT-TRE); and an
                                                                                                            Gene therapy, vector; prostate tumor; cytostatic; vasotropic; vulnerary; antipsoriatic; antimicrobial; immunomodulator; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New replication competent adenovirus vector comprising an inducible transcriptional transactivator coding sequence and an adenovirus gene, useful for treating cancer, psoriatic lesions, restenosis or wound
                                                                                                                                                                                                                        /product= "Adenovirus death protein"
                                                                                Adenovirus death protein coding sequence.
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ADW47774 standard; DNA; 307
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100.0%; Score 307; DB 14; Length 307; 100.0%; Pred. No. 2.4e-94;

Query Match Best Local Similarity

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TT, where the TT is functionally responsive to an exogenous inducer agent. The adenovirus gene is preferably a gene essential for adenoviral replication. The TT may be inhibited or activated by the inducing agent. Also claimed is an adenovirus vector comprising: an inducible TT coding sequence under the transcriptional control of a CT-TRE; and an adenovirus gene under transcriptional control of a RE regulated by the TT and a second gene under transcriptional control of a gecond gene may an adenovirus for a sectivated by an exogenous inducing agent. The second gene may an adenovirus fone embodiment of the invention provides adenovirus control of a sectivated by an adenovirus gene is under transcriptional control of a first transactivated regulated TRE and a polymucleotide encoding an ADP conders of a second transactivator regulated TRE, where the adenovirus gene is essential for replication. Also claimed are host cells comprising the replication competent adenovirus vector, and methods for propagating and regulating the vector. A claimed method for selective cytolysis of a target tumor cell line involves introducing the adenovirus coetor into a call which allows the CT-TRE to function, and administering an inducing agent such that the adenovirus vector can also be used to treat psoriatic lesions, resistance to infection, propagated and requising investigation of metabolic or other physical parhabove.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               physiological pathways, or comparison of activity of cells in the presence and absence of the virus introduced transgene. In vectors of the invention, expression of a viral gene essential for replication is regulated both by the CT-TRE and the transactivator regulated TRE, and
control of a TRE regulated by the
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Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

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                                                             GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT 60
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chemotherapy, cytosine deaminase; SR39; herpes simplex virus type 1;
thymidine kinase; death protein gene; cancer; neoplasm; 5-fluorocytosine;
                                                                                                                    Partial DNA sequence of AdS-yCD/mutTK(SR39)rep-ADP virus (E3 region).
                           BP
                           ADW28317 standard; DNA; 917
                                                                                       (first entry)
                                                                                       07-APR-2005
                                                         ADW28317;
RESULT 15
              ADW28317
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The specification describes a polynucleotide comprising a nucleotide sequence of yeast cytosine deaminase/mutant SR39 herpes simplex virus type 1 thymidine kinase fusion gene, and further comprising an adenovirus type 5 adenovirus death protein gene. The polynucleotide of the invention limits the side effects of cancer treatment by using only lower doses of radiation. The polypeptide encoded by the above polynucleotide is useful for converting 5-fluorocytosine or ganciclovir into active chemotherapeutic agents. Pharmaceutical compositions comprising useful for treating a mammalian patient having a malignancy or solid tumor. The present sequence represents a partial sequence (the E3 region) Novel isolated polynucleotide comprising nucleotide sequence of yeast cytosine deaminase/mutant SR 39 herpes simplex virus type 1 thymidine kinase fusion gene, useful for treating mammalian patient having malignancy or solid tumor. polynucleotide of the olnant adenovirus comprising the polynucleotid The recombinant adenovirus is designated Ad5ganciclovir; Ad5-yCD/mutTK(SR39)rep-ADP; 88. Barton K, Paielli D; Example; SEQ ID NO 3; 62pp; English. (FORD-) FORD HEALTH SYSTEM HENRY 09-JUL-2004; 2004WO-US022320. 09-JUL-2003; 2003US-0486219P of a recombinant adenovirus /CD/mutTK(SR39)rep-ADP Human adenovirus type Kim JH, WPI; 2005-101983/11 WO2005007109-A2. Freytag SD, 27-JAN-2005 Synthetic. 

240 120 180 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300 481 541 601 661 9 CARGIGGIGGITTITCCATAGGGCTTATGTTIGTITIGCCTTATTATTATGTGGCTTATTIG TTGCCTAAAAGCGCAGACGCCAGACCCCCCCATCTATAGGCCTATCATTGTGCTCAACCC 422 GATGACCGGCTCAACCATCGCCCCACAACGGACTATCGCAACACCACTGCTACCGGACT 482 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA CATGIGGIGGITITICCATAGCGCTTAIGITITGCTTTGCCTTATTATTATGTGGCTTATTTG 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 1 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT Gaps .; 0 Indels 100.0%; Score 307; DB 14; 100.0%; Pred. No. 4.1e-94; ive 0; Mismatches 0; Local Similarity 100. 121 542 181 602 241 셤 g 원 ਨੇ 셤 ò ò ઠે ò

Length 917;

Sequence 917 BP; 236 A; 223 C; 194 G; 264 T; 0 U; 0 Other;

Query Match

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Search completed: January 20, 2006, 19:29:31

Job time : 477 secs

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J01917 Adenovirus
AJ293913 Human ade
AL293915 Human ade
AL861085 Sequence
YL6037 Adenovirus
AX259967 Sequence
AX26362 Sequence
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AX084504 Sequence
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Henderson, D.R., Schuur, E.R. and Yu, D.-C.
Adenovirus vectors specific for cells expressing androgen receptor and methods of use thereof Patent: US 6197293-A 21 06-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
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Sequence 21 from patent US 6197293.
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/mol_type≈"unassigned DNA"
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AX770200
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AY339865
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AX262362
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AR628961
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AR451740 Sequence
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AR45174 Sequence
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AR45129 Sequence
AR5212 Human ade
AZ293912 Human ade
AZ293914 Human ade
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AZ293914 Human ade
                                                          ; Search time 2114 Seconds (without alignments) 8254.938 Million cell updates/sec
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                                                                                                                  1 gatgaccggctcaaccatcg......ttcttttacagtatgattaa 307
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        GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                             5883141 segs, 28421725653 residues
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Listing first 45 summaries
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and methods of use thereof

Patent: JP 2001515351-A 21 18-SEP-2001;

CALYDON INC

OS Unidentified

N JP 2001515351-A/21

PD 18-SEP-2001

PF 03-MAR-1998 US 60/039762,02-MAR-1998 US 09/033333 PI

PF 03-MAR-1997 US 60/039762,02-MAR-1998 US 09/033333 PI

DE CHAO YU, DANIEL R HENDERSON, ERIC R SCHUUR, HENRY G LAMPARSKI PC
C12N15/86,C12N5/10,A61K48/00,A61K47/48,C12Q1/70,C12N11/08 CC
Strandedness Single;
CC Topology: Linear;
CC Adenovirus vectors specific for cells expressing androgen CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adenovirus vectors containing heterologous transcription regulatory elements and methods of using same.
BD195488
BD195488.1 GI:33005258
JP 902514074-A/9.
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Best Local Similarity 100.0%; Pred. No. 1e-83;
Matches 307; Conservative 0; Mismatches 0; Indels 0
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/organism='Unidentified'
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Little, A.S., Henderson, D.R., Schuur, E.R. and Lamparski, H.

Little, A.S., Henderson, D.R., Schuur, E.R. and Lamparski, H.

Adenovirus vectors specific for cells expressing alpha-fetoprotein and methods of use thereof

Patent: US 6254862-A 22 03-JUL-2001;

Location/Qualifiers
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Yu,D.C., Henderson,D.R., Schuur,E.R. and Lamparski,H.G.
Adenovirus vectors specific for cells expressing androgen receptor
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Sequence 22 from patent US 6254862.
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JP 2001515351-A/21.
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1 (bases 1 to 307)
Little,A.S., Lamparski,H.G., Henderson,D.R. and Schuur,E.R.
Little,A.S., Lamparski,H.G., Henderson,D.R. and Schuur,E.R.
Adenovirus vector specific to cell expressing alpha-fetoprotein and method of using the same
Patent: JP 2002516568-A 22 04-JUN-2002;
CALYDON INC
S. Artificial Sequence
PN JP 2002516568-A/22
PD 04-JUN-2002
PN 03-MAR-1998 JP 1998538676
PR 03-MAR-1999 US 60/039597,02-MAR-1998 US 09/033428 PI
ANDREW S. LITLE,HENRY G. LAMPARSKI, DANIEL R. HENDERSON, ERIC R. PI
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CI2N15/86,CI2N5/10,A61K48/00,A61K47/48,CI2Q1/70,CI2N11/08
Strandedness: Double;
CT Topology: Linear;
CC Adenovirus vectors specific for cells expressing CC
carcinoembryonic antigens
CC and methods of use thereof
FH CDS 2.304.
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Pred. No. 1e-83;
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1 (bases 1 to 307)
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                                                                                                                                                                                                                 /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 2002516568-A/22.
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Lamparski, H.G., Henderson, D.R. and Schuur, E.R.

LE Adenovirus vectors specific for cells expressing carcinoembryonic antigens and methods of use thereof

NAL Patent: JP 2002514075-A 19 14-MAY-2002;

CALYDON INC

OS Unidentified

PR JP 2002514075-A ---

PR JP 2002514075-A ---

PR JA-W----
                                                                                                               Strandedness:
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G LAMPARSKI, DANIEL R HENDERSON, ERIC R SCHUUR PC
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PD 14-MAY-2002
PF 03-MAR-1998 JP 1998538674
PR 03-MAR-1999 US 60/039762,03-MAR-1997 US 60/03976.
PR 03-MAR-1997 US 60/03976.
PR 04-MAC-1997 US 60/03556 PI
R HENDERSON DE CHAO YU, HENRY G LAMPARSKI PC
C12N15/86,C12N5/10,A61K48/00,A61K47/48,C12N11/08 CC Stran single;
CC Topology: Linear;
CC Adenovirus vectors containing heterologous transcripti
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/ organism="unidentified"
/mol type="genomic DNA"
/db_xref="taxon:32644"
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Adenovirus vectors containing cell status-specific response
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CI2N15/09,A61K48/00,A61P35/00,C12N1/15,C12N1/19,C12N1/21,C12N5/
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Yu, D.C. and Henderson, D.R.
Adenovirus vectors containing cell status-specific response elements and methods of use thereof Patent: JP 2002525063-A 8 13-AUG-2002;
CALYDON INC
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                                                                                          Query Match 100.0%; Score 307; DB 6; Length 307; Best Local Similarity 100.0%; Pred. No. 1e-83; Matches 307; Conservative 0; Mismatches 0; Indels
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10-SEP-1999 JP 2000570347
10-SEP-1999 US 60/099791,09-SEP-1999 US
CHAO YU, DANIEL R HENDERSON
                      /organism="synthetic construct"
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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1 (bases 1 to 307)
Henderson, D.R., Schuur, B.R. and Yu, D.-C.
Henderson, D.R., Schuur, B.R. and Yu, D.-C.
Adenovirus vectors specific for cells expressing androgen receptor and methods of use thereof
Patent: US 6436394-A 21 20-AUG-2002;
Cell Genesys, Inc.; Foster City, CA
Location/Qualifiers
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241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
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100.0%; Score 307; DB 6; Length 307;
Best Local Similarity 100.0%; Pred. No. 1e-83;
Matches 307; Conservative 0; Mismatches 0; Indels C
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Sequence 21 from patent US 6436394.
AR223335.1 GI:23331486
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/mol_type="genomic DNA"
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PAT 20-FEB-2004
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1 (bases 1 to 307)

1 (bases 1 to 307)

Thenderson, D.R. and Schuur, B.R.

Tissue specific adenoviral vectors

Patent: US 6676935-A 61 13-JAN-2004;

Cell Genesys, Inc.; South San Francisco,
Patent: US 6676935-A 10 13-JAN-2004;
Cell Genesys, Inc.; South San Francisco,
Location/Qualifiers
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100.0%; Score 307; DB 6;
Best Local Similarity 100.0%; Pred. No. 1e-83;
Matches 307; Conservative 0; Mismatches 0
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Sequence 61 from patent US 6676935.
AR451740.
AR451740.1 GI:42682855
                                                                           /organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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Little, A.S., Henderson, D.R., Schuur, E.R. and Lamparski, H.
Little, A.S., Henderson, D.R., Schuur, E.R. and Lamparski, H.
Adenovirus vectors specific for cells expressing alpha-fetoprotein
and methods of use thereof.
Patent: US 6585968-A 22 01-JUL-2003;
Cell Genesys, Inc.; Poster City, CA
Location/Qualifiers
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                241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTTACAGTA 300
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ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTTTTTACAGTA 300
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Best Local Similarity 100.0%; Pred. No. 1e-83;
Matches 307; Conservative 0; Mismatches 0; Indels (
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Sequence 10 from patent US 6676935.
AR451690
AR451690.1 GI:42682805
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Sequence 22 from patent US 6585968.
AR349303
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Unclassified.
1 (bases 1 to 307)
Henderson, D. R. and Schuur, B.R.
Tissue specific adenoviral vectors
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241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
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                              1 (bases 1 to 307)
Yu, D.-C., Zhang, H. and Henderson, D.R.
Human and mouse uroplakin II gene transcriptional regulatory
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100.0%; Score 307; DB 6; Length 307;
Best Local Similarity 100.0%; Pred. No. 1e-83;
Matches 307; Conservative 0; Mismatches 0; Indels
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Unclassified.
1 (base 1 to 307)
Yu,D.C. and Henderson,D.R.
Adenovirus vectors containing cell statu
elements and methods of use thereof
Patent: US 6900049-A 7 31-MAY-2005;
Cell Genesys, Inc.; San Francisco, CA
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Best Local Similarity 100.0%; Pred. No. 1e-83;
Matches 307; Conservative 0; Mismatches C
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                                                                                             Patent: US 6852528-A 3 08-FEB-2005;
Cell Genesys, Inc.; San Francisco, CA
Location/Qualifiers
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Sequence 7 from patent US 6900049.
AR669908
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/mol_type="genomic DNA"
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                                     181 TTGCCTAAAGCGCAGACGCCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC 240
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                                                                                   ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300
                                                                                                    241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300
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Yu,D.-C., Li,Y., Little,A.S. and Henderson,D.R.
Cell-specific adenovirus vectors comprising an internal ribosome entry site
Patent: VS 6692736-A 17 17-FEB-2004;
Cell Genesys, Inc.; South San Francisco, CA
Location/Qualifiers
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AR474487
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Sequence 3 from patent US 6852528.
AR635125 GI:59793252
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/mol_type="genomic DNA"
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Best Local Similarity 100.
Matches 307; Conservative
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